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(54) Title: T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF USING SAME

(57) Abstract

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

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T-TYPE VOLTAGE-GATED CALCIUM
CHANNELS AND METHOD OF USING SAME

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER
FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

TECHNICAL FIELD OF THE INVENTION

The present invention relates to cloned T-type calcium channels.

BACKGROUND OF THE INVENTION

Biological membranes are themselves generally impermeable to ionic species. Thus. ions enter cells through regulated pores formed from membrane-associated proteins. Most of these regulated pores are voltage-dependent and are thus able to transduce changes in the transmembrane potential into ion flux. Voltage-gated ion channels form a "superfamily" of related proteins (cf. Jan et al., *Nature, 345,* 672 (1990)). Peculiar to this genus is a high degree of conservation in molecular structure. Generally, voltage-gated channels are membrane bound glycolsylated proteins formed of many subunits. Large α subunits form a pore in the membrane that is selective for a given ionic species. Each α subunit contains four domains (I, II, III, and IV). Each channel domain has six putative transmembrane helical segments (S_1-S_6). In general, the segments within each domain are similar but not identical. Aside from overall structural conservation, certain charged residues within the domains are highly conserved among voltage-gated ion channels (Jan et al., *supra*; Stühmer et al., *Nature, 339,* 597-603 (1989)).

Differences in charged residues between groups of voltage-gated ion channels confer properties unique to each subgroup, such as ion selectivity. For example, most voltage gated ion channels are selective for either sodium, potassium or calcium. Known calcium channels require a ring of negative charge provided by glutamate residues found at similar locations in each of the domains (Yang et al., *Nature, 366,* 158-61 (1993)).

Voltage-gated channels are often classified on the basis of their electrophysiology. The resting membrane potential of most animal cells is between about -70 mV and -80 mV. When the membrane becomes depolarized (moved towards 0 mV), various membrane channels become activated (they are said to

"open"). Thus, one basis for classifying membrane channels is the membrane potential necessary to activate (or "gate") them (voltage dependency). For example, "T-type" calcium channels are activated at a lower voltage than L- or N-type channels (Nowycky et al., *Nature, 316,* 440-43 (1985)). Other physiological properties are the activation kinetics, inactivation kinetics, tail current (deactivation kinetics), and single channel conductance. Thus, in comparison to other calcium currents, T-type calcium current is characteristically short (Chen et al., *J. Gen. Physiol., 96,* 603-30 (1990)), and it exhibits characteristically slow activation kinetics near threshold, fast inactivation kinetics, and slow tail current (Randall et al., *Neuropharmacol., 63,* 879-93 (1997); Carbone et al., *Nature, 310,* 501-02 (1984); Nilius et al., *Nature, 316,* 443-46 (1985)).

Calcium currents have been implicated in many neurological and muscular functions. For example, T-type calcium current is associated with cardiac pacemaker activity, pain transmission in the central nervous system, and in other physiological functions. Defects in T-type calcium current have been implicated in cardiac arrhythmia, hypertension, and epilepsy. Given their potential clinical value, the pharmacological properties of calcium channels have been the subject of extensive study. Most such studies have involved L-type channels because, unlike T-type channels, L-type calcium channels are readily purified from cell extracts. For example, L-type calcium channels have been purified using dihydropyridine drugs (e.g., nifedipine) which can bind with sufficiently high affinity to serve as a ligand for purifying L-type calcium channels. Such purified and cloned L-type calcium channels have been used to develop assays for drugs affecting L-type calcium channels (see, e.g., U.S. Patents 5,429,921 and 5,386,025).

While many electrophysiological characteristics of T-type calcium currents are known, the lack of isolated T-type channels has stalled research into the pharmacology and biophysics underlying the T-type calcium current, at least in comparison with other calcium channels. Indeed, while it is generally assumed that voltage-sensitive ion channels are responsible for the current, no such channel protein, nor any nucleic acid encoding such a protein, has been isolated. In view of the foregoing problems, there exists a need for an isolated T-type calcium channel and a nucleic acid encoding a T-type calcium channel.

BRIEF SUMMARY OF THE INVENTION

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or

substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

The present invention is useful for exploring the electrophysiology and pharmacology of the T-type calcium current. Such knowledge can lead to the development of drugs for potentiating or attenuating T-type calcium channels. Thus, the present invention provides an assay for identifying potential drugs affecting T-type calcium channels by exposing cells expressing a T-type calcium channel to a putative drug and then measuring the calcium flux in response to a change in membrane potential. The identification of drugs affecting T-type calcium channels will facilitate even greater understanding of the biophysics of these proteins. Furthermore, some such drugs could have potential clinical applications.

The invention can best be understood with reference to the accompanying drawings and in the following detailed description of the preferred embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E compare the complete amino acid sequences of three types of T-type calcium channels ($\alpha 1G$ (or $Ca_vT.1$), $\alpha 1H$ (or $Ca_vT.2$), and $\alpha 1I$ (or $Ca_vT.3$)), indicating conserved functional domains.

Figures 2A-2D are graphic representations of the current-voltage relationships of three cloned T-type calcium channels (Figures 2A, 2B, and 2C) and a cloned R-type calcium channel (Figure 2D).

Figure 3A is a graphic representation of the average current-voltage curve for cloned T-type calcium channels ($\alpha 1G$, triangles, $\alpha 1H$, inverted triangles, $\alpha 1I$, circles), and a cloned R-type calcium channel (filled squares). Figure 3B compares the normalized conductance of a cloned T-type calcium channel at three different concentrations of $BaCl_2$.

Figure 4 depicts average kinetics of the tail current as a function of repolarization potential for $\alpha 1G$ (triangles), $\alpha 1H$ (inverted triangles), $\alpha 1I$ (circles), and a cloned R-type calcium channel (filled squares).

Figures 5A and 5B graphically present data concerning the use of a cloned T-type calcium channel to detect drugs affecting the channel. Figure 6A depicts the effect of 100 µM on current-voltage relationships with a single dosage of miberfradil. Figure 6B illustrates the effect on T-type channel conductance of various doses of miberfradil.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α

subunit. The nucleic acid can be of any type, and it can include other elements aside
from a sequence encoding a T-type calcium channel domain or domains. For
example, where the nucleic acid comprises RNA, it can also include regulatory
sequences suitable to permit translation of the RNA. Thus, an RNA nucleic acid of
the present invention preferably has at least one ribosome entry site, and preferably
has a polyadenosine tail for stabilizing the RNA in the cellular environment.
Similarly, DNA nucleic acids of the present invention can have regulatory elements
for promoting the transcription of sequence encoding the T-type calcium channel into
an RNA such as that described above. For example, a DNA nucleic acid of the
present invention can have a promoter and/or an enhancer sequence. While the
nucleic acid can be any type of nucleic acid, the nucleic acid preferably comprises a
cDNA. A cDNA nucleic acid is preferred over other nucleic acids to permit the
nucleic acid to be readily cloned, sequenced, and expressed in a wide variety of cells.

The choice of promoter and/or an enhancer will largely depend on the milieu in
which the nucleic acid is to be expressed. Thus, for expression in bacterial cells, the
regulatory elements are bacterial promoters. Similarly, for expression in mammalian
cells, the regulatory elements are able to effect expression in mammalian cells. While
many such regulatory elements are known in the art, examples include prokaryotic
promoters and viral promoters (e.g., retroviral ITRs, LTRs, immediate early viral
promoters (IEp), such as herpesvirus IEp (e.g., ICP4-IEp and ICP0-IEp),
cytomegalovirus (CMV) IEp, and other viral promoters, such as Rous Sarcoma Virus
(RSV) promoters, and Murine Leukemia Virus (MLV) promoters). Other suitable
promoters are eukaryotic promoters, such as enhancers (e.g., the rabbit β-globin
regulatory elements), constitutively active promoters (e.g., the β-actin promoter, etc.),
signal specific promoters (e.g., inducible promoters such as a promoter responsive to
RU486, etc.), and tissue-specific promoters (e.g., those active in epidermal tissue,
dermal tissue, tissue of the digestive organs (e.g., cells of the esophagus, stomach,
intestines, colon, etc., or their related glands), smooth muscles, such as vascular
smooth muscles, cardiac muscles, skeletal muscles, lung tissue, hepatocytes,
lymphocytes, endothelial cells, sclerocytes, kidney cells, glandular cells (e.g., those in
the thymus, ovaries, testicles, pancreas, adrenals, pituitary, etc.), tumor cells, cells in
connective tissue, cells in the central nervous system (e.g., neurons, neuralgia, etc.),
cells in the peripheral nervous system, and other cells of interest).

The isolated or substantially purified nucleic acid of the present invention
encodes all or part of a T-type calcium channel α subunit. As used herein, a "calcium
channel" includes a protein structure for facilitating the flux of calcium ions across a
biological membrane into which the calcium channel is inserted. As used herein, a
"T-type channel" is a type of voltage-gated ion channel that facilitates the flux of ions

when the membrane potential of a biological membrane into which it is inserted experiences a slight depolarization. Thus, a T-type calcium channel can begin to gate from about -60 mV to about -30 mV (i.e., about -45 mV to about -35 mV) in about 10 mM Ba^{2+}. Additionally, T-type channels of the present invention exhibit a slow deactivation (tail current) following depolarization. Thus, a T-type calcium channel can exhibit a tail current that decays exponentially with a tau value from about 1 ms to about 10 ms (e.g., from about 4 ms to about 7 ms, such as about 6 ms) following repolarization to a membrane potential from about −80 mV to about −60 mV in a solution with a Ba^{2+} concentration of from about 10 mM to about 40 mM. Another defining characteristic of T-type calcium channels is that they exhibit small single channel conductance. Thus, for example, a T-type channel exhibits a single channel conductance of from about 4 pS to about 12 pS (e.g., from about 6 pS to about 10 pS), and typically from about 7 pS to about 9 pS in a solution with a Ba^{2+} concentration of about 0.1 M.

The isolated or substantially purified nucleic acid of the present invention encodes all or part of any T-type calcium channel having at least one of the aforementioned electrophysiological properties when properly assembled within a cellular membrane. The general structure of calcium channels is summarized above and is otherwise known in the art. Thus, for example, the nucleic acid can encode one of the four functional domains mentioned above. As used herein, a domain of a T-type calcium channel is any protein structure able to associate with three other domains to form a tetrameric body functioning as a T-type calcium channel. While the native T-type calcium channel structure includes all four domains in a single polypeptide (indicated in Figures 1A-1E), a domain can exist as a polypeptide species separate from those containing the other domains. Such separate domains are able to associate within the plasma membrane to form a functional channel. Alternatively, where a plurality of domains are linked within a common polypeptide, the linkage can deviate substantially from the native linkage. Thus, for example, the domains can be linked by polypeptide sequences other than those sequences linking the domains in the native protein (e.g., non-native polyglutamate linkages). Indeed, the domains themselves can include non-native linkages between membrane-spanning elements within the domains. Aside from these modifications, the nucleic acid can encode a chimeric calcium channel domain (or an entire channel) comprising a portion of a T-type calcium channel and a portion derived from another calcium channel (or other channel) protein. For example, the chimera can include portions of domains from T-type channels responsible for low voltage gating and portions of domains from other calcium channels responsible for slow inactivation. Such a protein exhibiting T-type gating but longer inactivation kinetics would facilitate pharmacological research.

As mentioned. nucleic acids of the present invention can encode an entire T-type channel (i.e., a T-type channel protein comprising four functional domains). It has been discovered that at least three genes encoding T-type calcium channels exist in humans and rats (i.e.. $\alpha 1G$ (or $Ca_vT.1$). $\alpha 1H$ (or $Ca_vT.2$), and $\alpha 1I$ (or $Ca_vT.3$)). and alternate splicing of these isoforms exist. Examples of the amino acid sequences of full-length T-type channels. and the sequences of suitable coding nucleic acids are set forth at SEQ ID NOs:1-8 ($\alpha 1G$ sequences). SEQ IS NOs:9-10 ($\alpha 1H$ sequences), and SEQ ID NOs: 11-12 ($\alpha 1I$ sequences). However, the invention is not limited to these exemplary sequences. Indeed. as mentioned, an amino acid sequence of a T-type calcium channel can vary from those listed. and it is within the state of the art to change a nucleotide sequence encoding a T-type channel to introduce mutations into the protein. Indeed, for conducting electrophysiological assays, it may be desirable to introduce mutations into such a protein. For example, mutations comprising insertions or deletions can be introduced on either the amino- or carboxy-terminus of the protein, or such mutations can be intrasequence insertions or deletions. Where the electrophysiological properties of the calcium channel are to be conserved, such mutations preferably are in regions other than the membrane spanning domains. However, in some applications (e.g., to decrease inactivation kinetics), the changes can be within the membrane-spanning regions. Moreover, as mentioned above, the sequence can form a protein having only one functional domain of a T-type calcium channel. Additionally, the sequence can also form a chimeric protein or domain, such as those described above.

Aside from insertions and deletion mutations of native T-type calcium channel sequences. a T-type calcium channel can include substitutions of amino acid residues, e.g., for those indicated in SEQ ID NOs:1-12. Preferably, and especially where such a substitution is within a membrane spanning region, the substitution is conservative. Thus, within membrane spanning domains, positively-charged residues (H, K, and R) preferably are only substituted with positively-charged residues; negatively-charged residues (D and E) preferably are only substituted with negatively-charged residues; neutral polar residues (C, G, N, Q, S, T, and Y) preferably are only substituted with neutral polar residues; and neutral non-polar residues (A, F, I, L, M, P, V, and W) preferably are only substituted with neutral non-polar residues. Preferably, any amino-acid substitution within the membrane-spanning regions does not alter this conservation. Most preferably, any substitution, deletion, or insertion does not alter the IVS4 domain. In each of the exemplary T-type calcium channel α subunit sequences, the putative IVS4 region comprises SEQ ID NO:13. Given the strong sequence conservation among families of voltage-gated ion channels, it is likely that this sequence or a derivative sequence, will be present in T-type channels. Thus, the

present invention provides any T-type calcium channel (or a nucleic acid encoding such a T-type calcium channel) comprising SEQ ID NO:13 or a sequence derived from SEQ ID NO:13 having conservative amino acid substitutions. as described above.

5   The nucleic acid of the present invention encoding all or a part of a T-type calcium channel can be isolated via any suitable method. For example, prior to the present invention, one of skill in the art could design a probe based on the sequence of known, non-T-type, calcium channels and use such probe to screen a genetic library. If such a screen were to identify a putative calcium channel, the researcher could then
10   attempt to clone the entire nucleic acid to characterize it. Similarly, prior to the present invention, to isolate a nucleic acid encoding a T-type calcium channel, one of skill in the art could consult publicly available databases containing DNA sequences (e.g., Genbank) to locate nucleic or amino acid sequences representing a portion of a T-type calcium channel protein or nucleic acid. However, such databases contain no
15   sequence for a full-length T-type calcium channel or identify any sequence as a T-type channel. Such methods assume that T-type calcium channels share sufficient sequence identity with known calcium channel nucleic acids to cross-hybridize, an assumption not supported by any published report. Moreover, prior to the present invention, no partial sequence in such databases was identified as corresponding to a
20   T-type calcium channel. Thus, prior to the present invention, the presence of partial sequences in the public DNA databases could facilitate the isolation of T-type calcium channels only with the exercise of a considerable degree of speculation on the part of the researcher.

          By providing several sequences pertaining to T-type calcium channels and a
25   comparison presenting conserved regions and domains, the present invention greatly facilitates the isolation of other nucleic acids encoding T-type calcium channels (or derivatives thereof) with much less experimentation. Thus, while any of the methods discussed above can be employed to isolate other members of this genus, preferably, a nucleic acid encoding a T-type calcium channel is isolated by probing a genetic library
30   using a probe that hybridizes to a DNA encoding a peptide sequence contained in (or similar to) a known T-type calcium channel (e.g., SEQ ID NOs:1-12). To facilitate the isolation of a T-type calcium channel, the present invention provides an isolated polynucleotide hybridizing to a portion of the nucleic acid of the present invention encoding a T-type calcium channel (or a portion thereof). Thus, for example, the
35   present invention includes an isolated polynucleotide hybridizing to SEQ ID NO:1-12. The isolated polynucleotide can hybridize to all or any portion of the sequence encoding the T-type calcium channel.

To isolate such a polynucleotide. any portion of a sequence encoding a T-type calcium channel can be employed as a probe to screen a genetic library. and such screening can be accomplished by standard techniques known in the art. While the probe can hybridize to any portion of such a DNA, preferably the probe is designed to
5   hybridize to a DNA encoding a polypeptide sequence that is highly conserved among T-type calcium channels but is less conserved between the genus of T-type calcium channels and other proteins. Such peptide sequences are readily apparent from the sequence comparison set forth in Figures 1A-1E. Generally, the specificity of hybridization in a genetic screen varies depending on the length of the probe and the
10   stringency (e.g., temperature, salt and detergent concentration, etc.) of hybridization. Stringency of hybridization is broadly classified as "high," "moderate," or "low," and the parameters of these terms are well recognized in the art (see, e.g., Sambrook et al.. "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Press, 1989). The isolated polynucleotide hybridizing to a portion of the nucleic acid encoding a T-type
15   calcium channel can hybridize under any desired stringency conditions. However, for identifying other T-type channels, preferably, the hybridization occurs under moderate stringency, and most preferably under high stringency.

Of course, the isolated or substantially purified polynucleotide can itself be employed as a probe to screen a library as described to isolate a second nucleic acid.
20   In such a screen, one of the polynucleotides will be complementary to a portion of the sequence encoding the T-type calcium channel, and the other isolated nucleic acid will be "sense." Preferably, one of the two isolated polynucleotides (the "sense" strand) itself encodes a T-type calcium channel, or at least one domain thereof. Such a sequence can be cloned to be operably linked to suitable regulatory elements, as
25   described, to produce a T-type calcium channel. Thus, aside from using the nucleic acid of the present invention to produce a T-type calcium channel, the nucleic acids of the present invention are also useful for isolating other sequences encoding T-type calcium channels, or derivatives thereof.

However isolated, the isolated or substantially purified nucleic acid of the
30   present invention is useful, in part, for producing all or a portion of a T-type calcium channel. Thus, the nucleic acid can be introduced into a suitable milieu for driving its expression. Because T-type channels are transmembrane proteins, preferably such a milieu is a living cell. However, it should be understood that the nucleic acid can also be expressed *in vitro* under conditions, such as those known in the art, suitable for *in*
35   *vitro* transcription and translation. However produced, the present invention includes any protein, such as a recombinant protein or an isolated or substantially purified protein. including all or a portion of a T-type calcium channel or a protein derived from a T-type calcium channel.

For expression in a living cell, the nucleic acid must be introduced into the cell. As nucleic acids are generally introduced into cells as part of genetic vectors, the present invention provides a vector having a T-type calcium channel nucleic acid of the type described above. Any type of vector suitable for introducing the nucleic acid

5   into a host cell is within the context of the present invention. Examples of such vectors include naked DNA and RNA vectors (such as oligonucleotides, plasmids, capped cRNA, etc.), viral vectors such as adeno-associated viral vectors (Berns et al., *Annals of the New York Academy of Sciences, 772.* 95-104 (1995)), adenoviral vectors (Bain et al., *Gene Therapy, 1,* S68 (1994)), herpesvirus vectors (Fink et al., *Ann. Rev.*

10   *Neurosci., 19,* 265-87 (1996)), packaged amplicons (Federoff et al., *Proc. Nat. Acad. Sci. USA,* 89, 1636-40 (1992)), pappiloma virus vectors, picornavirus vectors, polyoma virus vectors, retroviral vectors, SV40 viral vectors, vaccinia virus vectors, and other vectors. Once a given type of vector is selected, its genome must be manipulated for use as a background vector, after which it must be engineered to

15   incorporate exogenous polynucleotides. Such manipulations are known in the art.

The vectors of the present invention are useful for introducing a nucleic acid encoding all or a portion of a T-type calcium channel into a host cell. Thus, the present invention provides a cell into which the vector of the present invention has been introduced. The host cell can be any cell suitable for expressing the nucleic acid

20   (e.g., bacteria, insect cells, mammalian cells, etc.). The host cell can thus be *in vitro* or *in vivo.* Preferably the cells do not exhibit native T-type calcium current. A preferred cell type is HEK-293 cells because they contain genetic elements that facilitate the expression of transgenes from a variety of expression vectors. For facilitating electrophysiological recordings, oocytes (e.g., *Xenopus* oocytes) are

25   preferred, as they are large and readily handled.

The vector can be introduced into the cell in any manner suitable for the cell type and vector employed. In one embodiment, the vector can be used to prepare an RNA transcript *in vitro* (e.g., a capped cRNA) which is then introduced into the host cell by standard methods (such as injection). Such techniques are preferred when the

30   host cells do not actively transcribe DNA (such as oocytes). In other embodiments, a DNA vector is introduced into the cell such that it is transcribed within the cell. For example, the vector can be introduced into the cell such that it forms an extrachromosomal segment of genetic material in the cell, as is the case with many types of viral vectors. Alternatively, the vector can introduce the nucleic acid into the

35   chromosomal DNA of the host cell.

Preferably, a cell into which the nucleic acid is introduced is also able to express the nucleic acid to produce the α subunit protein. The expression of the nucleic acid can be detected by probing the cell for the presence of T-type calcium

channel mRNA. such as via Northern hybridization analysis. in situ hybridization. etc. More preferably, however, the cell is able to express the nucleic acid to produce the protein including all or a portion of a T-type calcium channel. In such cells. expression of the nucleic acid is confirmed by detecting the protein. for example, by

5   probing cellular extracts with an antibody recognizing the protein (e.g.. on a Western blot. etc.).

In the membrane of the cell producing the protein, the expressed protein contributes to the formation of a functional calcium channel. Where the protein encodes an entire α subunit. the full protein will possess some or all of the

10   electrophysiological properties of T-type calcium channels described above. Where the protein encodes less than an entire channel α subunit (e.g., a domain). the protein will aggregate with other constituent domains in the membrane to form a functional channel. Thus; the presence of the protein can be detected by assaying the cell for T-type calcium channel activity. Indeed, assaying for channel activity serves to

15   determine whether a nucleic acid encoding a putative calcium channel. in fact. encodes a species of T-type channel (as opposed to a member of another genus of calcium channels). For example. when large cells (e.g., oocytes) are used as the host cells, the electrophysiological properties of the channel can be investigated. Thus, the membrane activity of whole cells expressing the nucleic acid can be measured

20   directly, such as via patch clamp techniques using a voltage clamp electrode and a current electrode (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). Alternatively, the activity of single channels can be measured, such as with a standard depolarizing bath and pipette solutions (Lacerda et al.. *Biophys. J., 66*, 183-43 (1994)). However measured, the properties of cells into which the putative nucleic

25   acid is introduced are compared to the channel conductance, voltage dependency, activation kinetics, inactivation kinetics, or tail current known for T-type channels and discussed above. A measure of current density (e.g., pA/pF) can also be used to assess the level of gene expression in the cells, normalizing for cellular volume.

While, in accordance with the present invention, an isolated cell into which the

30   T-type calcium channel nucleic acid has been introduced (and preferably stably expressing the nucleic acid to produce the protein) can be prepared, preferably, such transfection protocols result in a population consisting essentially of such transfected cells. For standardizing the results of many experiments, it is even more desirable to employ an established cell line consisting essentially of such cells. Preferably, for use

35   in high throughput assays, cell lines stably expressing a T-type calcium channel exhibit a current density of at least about 40 pA/pF (e.g.. at least about 45 pA/pF). such as about 50 pA/pF or even 55 pA/pF or higher. Preferably, a cell line in accordance with the present invention is able to propagate the nucleic acid through

several passages (e.g.. for at least 10 passages). and. preferably. the nucleic acid is stably integrated into the chromosomes of such cells. Thus. the cell line can propagate the nucleic acid for at least 20 passages. and more preferably significantly more than 20 passages (e.g.. at least about 25 passages. or even more).

5   Regardless of the cell system. the ability to express a T-type calcium channel nucleic acid within host cells to produce an active channel permits the channel to be further studied. In this regard. the present invention provides a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel. as herein described.
10   The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter, the presence or absence of calcium flux in response to a change in membrane potential is assayed. Any such assay can be employed within the context of the present invention. (e.g.. using labile dyes, radioisotopes (e.g., ^{45}Ca). recording electrophysiological changes in the membrane,
15   etc.). A quick method of assaying for calcium flux is first to introduce a calcium-sensitive labile dye into the cells. For example. the dye can be one such as those that fluoresce or change color in the presence of calcium, many of which are known to those of skill in the art (e.g.. Indo-1). Thereafter, the cells are exposed to a depolarizing solution containing high (e.g., about 50 mM) potassium concentration
20   and a drug, and the reaction of the labile dye is compared to control cells. Using a labile dye affords the ability to assay many putative drugs quickly in a high throughput assay for putative drugs affecting T-type channels. For example, the initial screening can be carried out in 96 well plates. Moreover. dose-response data can be readily generated by exposing the cells to several concentrations of the same putative
25   drug.

        Once a putative drug is detected, its effect on the electrophysiology of the cell (e.g., single channel conductance, voltage dependency, activation kinetics, inactivation kinetics, and tail current of the cells) can be investigated in detail. Generally, the effect of the putative drug on T-type calcium currents is assessed by
30   measuring the various electrophysiological parameters in the presence of various concentrations of the drugs and comparing the data to untreated (or sham-treated) control cells. Cells preferably are maintained in a continuous perfusion chamber during such experiments to facilitate changing solutions. The inventive method of identifying a drug which affects T-type calcium channels can employ any nucleic acid
35   encoding a T-type calcium channel (or derivative thereof). such as those nucleic acids described herein. In fact, as several isoforms of T-type channel exist, the assay method can be repeated using nucleic acids encoding different isoforms to identify

drugs that preferentially target a given isoform. or drugs which affect more than one isoform of T-type calcium channels.

Aside from affording an *in vitro* assay for detecting potential therapeutic or investigative drugs targeting T-type calcium channels, the method of expressing the
5   T-type calcium channel nucleic acid can also be used *in vivo*. For example, as mentioned, several neurological and muscular diseases or disorders have implicated mutations affecting native nucleic acids encoding T-type calcium channels. The present invention, thus, provides a method of treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid. The method
10   involves introducing a vector having the T-type calcium channel nucleic acid into cells of a host in which native expression of the nucleic acid is deficient. Thus, for example, for treating cardiomyopathy associated with deficiencies in T-type calcium channels, the vector is introduced into myocardial cells. Similarly, for treating forms of epilepsy associated with deficiencies in T-type calcium channels, the vector is
15   introduced into neurons (e.g., thalamic neurons). Within the target cells, the nucleic acid within the vector is expressed to produce active T-type calcium channel. By similar methods, an nucleic acid having a sequence antisense to a sequence encoding a T-type calcium channel (or a portion thereof) can be expressed within a cell. The presence of an antisense sequence can down-regulate the expression of native T-type
20   calcium channel genes by hybridizing to T-type channel mRNA within the cell. Thus, the present invention is useful to treating disorders associated with over-expression of T-type calcium channels.

T-type channel proteins (such as whole T-type calcium channels, domains of such channels, chimeras including portions of T-type calcium channels, etc.) can be
25   employed to generate antibodies (e.g., immunoglobulins) to T-type calcium channels. Thus, the present invention provides an isolated and substantially purified antibody molecule recognizing an epitope on a T-type calcium channel. Such antibodies can be monoclonal antibodies or polyclonal antisera. Antibodies recognizing T-type calcium channels can be used to purify the channels from cell extracts or other solutions by
30   standard methodologies (e.g., immunoprecipitation). Moreover, depending on the location of the epitopes for the antibodies on the T-type calcium channel, the antibodies can be used to affect the channel proteins present on the surface of cells. Thus, antibodies directed to T-type calcium channels are potential reagents for studying the channels as well as for therapy.

35   Such antibodies can be produced by any suitable method, many of which are well known in the art. Thus, for example, the antibodies can comprise polyclonal antisera obtained from innoculated animals. Alternatively, the antibody molecules can be monoclonal antibodies obtained from a cell line (e.g., a hybridoma cell line). Thus,

the present invention provides a cell which produces such antibodies. Such a cell can be *in vitro* or *in vivo*: however, where the cell is *in vitro*, preferably it is within an established cell line consisting essentially of such cells.

Several examples are presented below to illustrate the invention. Taken
5 together, the examples demonstrate the cloning of twelve novel proteins and their characterization as T-type calcium channel α subunits. These examples are included here for purely illustrative purposes; as such, they are not to be construed so as to limit the scope of any aspect of the invention.

Many procedures employed in the following examples are techniques routinely
10 performed by one of ordinary skill in the art (see generally Sambrook et al., *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)) and are not discussed in detail. However, some reagents and methods deserve specific description. Thus, for example, *in vitro* translation and expression were conducted as described previously (Schneider et al., *Receptors and Channels, 2*,
15 255-70 (1995)). *Xenopus laevis* oocytes were prepared as described previously (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). To express proteins, 10 or 30 ng of capped cRNA was injected into the oocytes in a volume of 50 nl. For single channel recording, oocytes were injected with 100 ng capped cRNA and incubated for one week prior to assay.

20 Cells were voltage clamped using a two-microelectrode voltage clamp amplifier as described (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). The standard bath solution contained the following: 40 mM $Ba(OH)_2$, 50 mM NaOH, 1 mM KOH, 0.1 mM EDTA, and 5 mM HEPES, adjusted to pH 7.4 with methanesulfonate. The osmolality of the 2 mM Ba^{2+} and 10 mM Ba^{2+} solutions was
25 balanced by increasing the NaOH concentration as described (Lory et al., *J. Physiol., (London), 429*, 95-112 (1990)). Voltage and current electrodes (1.5-1.8 M tip resistance) were filled with 3 M KCl. Except as noted, data were acquired at 4 kHz using the pCLAMP system, and filtered at 1 kHz. Data were analyzed using pCLAMP software. Boltzman fits and linear regression were calculated using Prism.
30

EXAMPLE 1

This example demonstrates the cloning and characterization of putative T-type calcium channels.

A search of the Genbank library was conducted to identify clones identified as
35 having some degree of homology to known calcium channel sequences. The search identified an expressed sequence tagged (EST) partial sequence in a human brain clone (H06096), which was used as a probe to screen a λgt10 cDNA library prepared

from rat brain. Successive screening of the cDNA library identified five overlapping clones which were aligned to construct an entire cDNA sequence, termed α1G.

The α1G cDNA was cloned into the pSP72™ vector and sequenced by standard computer-assisted sequencing. Using the α1G cDNA, the amino acid

5 sequence of the α1G protein was deduced and compared to the sequences of other known calcium channel α subunits. By similar methods, homologous human (H19230 and R19524) and mouse (AA286626) EST clones were also identified and partially sequenced, and alternately spliced variants were identified. The deduced cDNA and amino acid sequences for eight full-length α1G T-type channels are set

10 forth, respectively, as SEQ ID NOs:1-8.

A second T-type calcium channel, termed α1H, was isolated by screening a human heart cDNA library with a fragment of the α1G sequence. An alternately spliced isoform was also identified. The full-length cDNA and amino acid sequences for these α1H T-type channels are set forth, respectively, as SEQ ID NOs:9 and 10.

15 A third T-type calcium channel, termed α1I, was isolated by screening a rat brain cDNA library at low stringency using a fragment of the rat α1G gene. Fifty plaques were identified, many of which were not detected in a second screening. A third screening with a fragment from α1H identified two clones. Subsequent screening, and the use of the GenBank database, led to the identification of the full

20 length rat and human cDNA and amino acid sequences, set forth at SEQ ID NOs: 11 and 12, respectively.

The α1G, α1H, and α1I amino acid sequences were compared to each other and a known calcium channel (α1E) to investigate the conservation of protein structure and function. The comparison indicates that the α1G, α1H, and α1I amino

25 acid sequences within the putative membrane-spanning domains are about 90 % identical to each other, while the α1G, α1H, and α1I sequences are only roughly 40 % identical to the α1E clone.

Figures 1A-1E indicate this conservation between the proteins. The conservation of charged residues, particularly in the S4 domains, is consistent with the

30 role of the α1G, α1H, and α1I proteins as ion channels. However, two of the glutamates associated with ion specificity in other calcium channels have been replaced with aspartate, suggesting altered ion selectivity. Strikingly, α1G, α1H, and α1I display only low homology to sequences linking the membrane-spanning regions within each domain, and even less homology between the intracellular loops linking

35 domains. Notably, neither α1G, α1H, nor α1I possesses sequences known to bind β subunits or Ca^{2+} ions.

EXAMPLE 2

This example demonstrates the production of cell lines stably expressing the cloned α1G, α1H, and α1I proteins.

HEK-293 cells were transfected with either the rat α1G cDNA (SEQ ID NO:1), the human α1H cDNA (SEQ ID NO:9), or the rat α1I cDNA (SEQ ID NO:11). As a control, cells were also transfected with human α1E plus human β3 (Schneider et al., *Receptors Channels*, 2, 255-70 (1994); Murakami et al., *Eur. J. Biochem.*, 236, 138-43 (1996)). The DNA constructs included a neomycin resistance gene conferring resistance to G418. The cells were cultured under standard conditions using medium containing G418 to select for stable transformants.

Surviving clones were expanded and assayed for electrophysiological activity to determine the presence of channels within the membrane. Whole-cell currents were recorded from ruptured patches using an Axopatch 200A amplifier, Digidata 1200 A/D converter, and pCLAMP 6.0 software. Data were digitized at 2 kHz and filtered at 1 kHz or off-line. All experiments were performed at room temperature. Pipettes were made out of TW-150-6 capillary tubing (World Precision Instruments, Inc., Sarasota, FL), using a Model P-97 Flaming-Brown pipette puller (Sutter Instrument Co., Novato, CA). The internal pipette solution contained the following: 55 mM CsCl, 75 mM CsSO$_4$, 10 mM MgCl$_2$, 0.1 mM EGTA, 10 mM HEPES, pH adjusted to 7.2 with CsOH. The external Tyrodes solution was the following: 140 mM NaCl, 6 mM KCl, 2 mM CaCl$_2$, 10 mM glucose, 5 mM HEPES, pH 7.4. The recording solution contained the following: 10 mM BaCl$_2$ solution (or 2 mM CaCl$_2$), 140 mM tetraethylammonium (TEA) chloride, 5 mM CsCl, 1 mM MgCl$_2$, 5 mM glucose, and 10 mM HEPES, pH adjusted to 7.4 with TEA-OH. Under these solution conditions the pipette resistance was typically 1.5-2.5 MΩ. Cell capacitance was measured by integrating the charging current during a 10 mV hyperpolarizing pulse (holding potential -80 mV).

Using these recording techniques, values for pA/pF were obtained for each cell line, which is a measure of current density normalizing for cell size. One clone (#N2) expressed the rat α1G protein and has a current density of 42 pA/pF. Another clone (#13), expressed the human α1H protein and exhibited a current density of 53 pA/pF. Three clones (#11, #19, and #25) expressed the rat α1I protein and exhibited current densities of 40 pA/pF, 45 pA/pF, and 55 pA/pF, respectively

EXAMPLE 3

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type current-voltage relationships.

Current traces were elicited by depolarizing voltage clamp pulses of the membranes of cells. The α1G. α1H. and α1I proteins were produced in *Xenopus laevis* oocytes by linearizing the DNA vectors containing the coding sequences. and transcribing the coding sequences *in vitro* by standard methods. Oocytes were then injected with the capped RNA.

Figures 2A-2E depict data obtained from these experiments using cells injected with α1G (Figure 2A). α1H (Figure 2B). and α1I (Figure 2C) and α1E (Figure 2D). These data indicate that cells expressing α1G, α1H. and α1I exhibit T-type calcium current, while oocytes expressing α1E as well as uninjected oocytes (Figure 6A) do not.

Current voltage curves were developed using cells injected with α1G, α1H, α1I, and α1E. Figures 3A depicts such data generated in a 10 mM Ba^{2+} test solution. These data were transformed into conductance and fit with a Boltzman equation to determine the midpoint of activation ($V_{0.5}$). Gating potentials for α1G. α1H. and α1I (-38 ± 1 mV n=8, -44 mV ± 1 mV. n=10, and -31 mV ± 1 mV. n=6, respectively) were in accordance with the gating potential measured for the HEK-293 cells (-41 ± 1 mV, n=10). while α1E required significantly more positive potentials to open (-2.6 mV ± .4 mV, n=3).

To compare the characteristics with published values (Huguenard, *Ann. Rev. Physiol.*, *58*, 329-48 (1996)), the α1G current was recorded at varying concentrations of Ba^{2+}. As indicated in Figure 3B. in solutions containing 2 mM Ba^{2+}, $V_{0.5}$ was -46.5 mV. and the slope factor (*k*) was 6.6 (n=7). However, when the Ba^{2+} concentration was 40 mM, $V_{0.5}$ was recorded at -21 mV, presumably due to the results of barium on surface charge screening (see, e.g., Wilson et al., *J. Membrane Biol.*, *72*, 117-30 (1983)). Similar values were recorded for α1H and α1I.

These results indicate that α1G, α1H, and α1I are low-voltage activated calcium channels (i.e., from about -60 mV to about -30 mV in 10 mM Ba^{2+}).

EXAMPLE 4

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type tail current.

Tail current was measured at -90 mV after first opening the channels with a voltage step to -10 mV. The voltage-dependence of tail current in cells expressing α1G (oocytes) α1H (HEK 293 cells), and α1I (HEK 293 cells) was measured at varying test potentials. As a control, tail current was also measured from a high voltage activated channel α1E, which Raw data from recordings data were fit with a single exponential and plotted as a function of depolarization potential (Figure 4).

These results demonstrate that the tail currents for the cloned α1G. α1H. and α1I calcium channels are voltage-dependent. consistent with known T-type calcium tail currents. Additionally. these data demonstrate that the tail current for each of the cloned channels is between about 1 ms and about 10 ms following repolarization to a membrane potential from about –80 mV to about –60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

EXAMPLE 5

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type single channel conductance.

Measurement of single channel conductance is complicated by the low probability of channel opening at negative potentials when the driving force is large. Thus. single channel conductance was measured similarly for measurements of tail currents to enhance channel opening at negative potentials. Single channels were measured with standard depolarizing bath and pipette (115 mM $BaCl_2$. 1 mM EGTA. and 10 mM HEPES, pH 7.4) solutions (Lacerda et al., *Biophys. J.*, 66. 1833-43 (1994)). Data were analyzed with TRANSIT (VanDongan, *Biophys J.*, 70, 1303-15 (1996)). Single channel amplitudes were measured by averaging the values obtained from Gaussian fits to all-points histograms of traces with openings, selected openings, or amplitude histograms of idealized openings. It has been reported that some oocytes contain a native 9 pS channel. These endogenous channels can be distinguished by their 2-fold larger current amplitudes at the potentials tested (e.g., -20 mV, $i = 0.8$ for endogenous channels as opposed to 0.4 pA for α1G). However, such endogenous channels were not detected either at the whole cell or single channel level in the oocytes tested.

Current through the main open state of each open channel was measured at each potential and plotted against each test potential. Single channel currents for several patches were then averaged and plotted as a function of test potential, wherein the slope of the plot indicated the single channel conductance. The average slope conductance of the α1G channel was measured at 7.5 ± 1.5 pS, which corresponds with the reported values for T-type calcium channels (Hugenard, *Ann. Rev. Phsysiol.*, 58, 329-48 (1996)). Similar results were also obtained with both α1H (10.8 ± 1.4 pS). Data collected from recordings of the α1I channels indicate that they open to two distinct amplitudes. The conductance for the small amplitude α1I openings was measured at 3.9 ± 0.5 pS, while that for the large α1I openings was measured at 11.4 ± 0.5 pS).

These results indicate that the cloned α1G. α1H. and α1I proteins exhibit T-type single-channel conductance (e.g.. from about 4 to about 12 pS).

EXAMPLE 6

This example demonstrates that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels.

5   HEK-293 cells were subjected to treatment as indicated above in Example 3, except that an experimental group of cells were exposed to a solution containing 1 μM mibefradil, a known inhibitor of T-type calcium current. As depicted in Figure 5A, the presence of mibefradil almost completely abolished T-type current in cells expressing α1G. Cells expressing either α1G or α1H were similarly treated using

10   various concentrations of mibefradil to determine a dose-response relationship. These results, depicted in Figure 5B, demonstrate that about 50% inhibition was achieved at a mibefradil concentration of 1 μM.

All of the references cited herein, including patents, patent applications, and

15   publications, are hereby incorporated in their entireties by reference.

While this invention has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations of the preferred embodiments may be used and that it is intended that the invention may be practiced otherwise than as specifically described herein. Accordingly, this

20   invention includes all modifications encompassed within the spirit and scope of the invention as defined by the following claims.

What is claimed is:

1. A isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α subunit.

2. The nucleic acid of claim 1, wherein said protein comprises an entire T-type calcium channel α subunit.

3. The nucleic acid of claim 2, wherein said protein comprises SEQ ID NO:13.

4. The nucleic acid of any of claims 1-3, wherein said calcium channel begins to gate from about -60 mV to about -30 mV in 2 mM Ba^{2+}.

5. The nucleic acid of any of claims 1-4, wherein said calcium channel exhibits a tail current of from about 1 ms to about 10 ms following repolarization to a membrane potential from about −80 mV to about −60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

6. The nucleic acid of any of claims 1-5, wherein said calcium channel exhibits a single channel conductance of from about 4 pS to about 11 pS in a solution with a barium ion concentration of about 100 mM.

7. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of any of claims 1-6.

8. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of claim 7.

9. The nucleic acid of claim 8 comprising a sequence encoding at least one domain of a T-type calcium channel α subunit.

10. A vector comprising the nucleic acid of any of claims 1-9.

11. A cell into which the vector of claim 10 has been introduced.

12. The cell of claim 11, which expresses said nucleic acid to produce said protein.

13. The cell of claim 11 or 12, which stably expresses said nucleic acid to produce said protein.

14. A population of cells consisting essentially of cells according to any of claims 11-13.

15. An established cell line consisting essentially of cells according to any of claims 11-13.

16. A method of identifying a drug which affects T-type calcium channels, said method comprising expressing a T-type calcium channel in a cell, exposing said cell to a putative drug, and measuring the calcium flux through the membrane of said cell in response to a change in membrane potential.

17. The method of claim 16. wherein said calcium flux is assayed by using a calcium-sensitive labile dye within said cell.

18. The method of claim 16. wherein said calcium flux is assayed by measuring the electrophysiological properties of said cell.

19. The method of claim 16. wherein said calcium channel comprises SEQ ID NO:13.

20. An isolated or substantially purified immunoglobulin recognizing an epitope on a T-type calcium channel protein.

21. A cell *in vitro* which produces the immunoglobulin of claim 20.

22. An established cell line consisting essentially of cells according to claim 21.

```
                                                                                          IS3
hCavT1a  MDEEEDGAGAEESGQPR-----------------------------------SFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW
rCavT1a  MDEEEDGAGAEESGQPR-----------------------------------SFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW
hCavT2a  MTEGARAADEVRVPLGRRPWPCGVGGVPGEPRGAGTRGGGFELGVSPSESPAAERCAELGADEEQRVPYPALAATVFFCLGQTTRPRSWCLRLVCNPW
hCavT3   MAESASPPSSSAAA------------------------------PAAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPW
rCavT3   MADSNLPPSSAAAP------------------------------APEPG--ITEQPGPRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKMVCNPW


         IS1                                                IS2
hCavT1a  FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTV
rCavT1a  FERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTV
hCavT2a  FEHVSMLVIMLNCVTLGMFRPCEDVECGSERCNILEAFDAFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVVAGMEYSLDGHNVSLSAIRTV
hCavT3   FECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKIMQVFDDFIFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTV
rCavT3   FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTV


         IS4                                          IS5
hCavT1a  RVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRS
rCavT1a  RVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRS
hCavT2a  RVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDSAFVRNNNLTFLRPYYQTEEGEENPFICSSRRDNGMQK
hCavT3   RVLRPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYYQPEEDDEMPFICSLSGDNIMG
rCavT3   RVLRPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYYQPEEDDEMPFICSLTGDNGIMG


                                                              IP LOOP
hCavT1a  CRSVPTLRGDG------GGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFI
rCavT1a  CRSVPTLRGEG------GGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFI
hCavT2a  CSHIPGRRDVRMPCTLGWEA-YTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNTCYAWIAIFQVIFQVITLEGWVDIMYVMDAHSFYNFIYFI
hCavT3   CHEIPPLKEQGRECCLSKDDVYDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVIFQVITLEGWVEIMYYVMDAHSFYNFIYFI
rCavT3   CHEIPPLKEQGRECCLSKDDVYDFGAGRQDLNASGLCVNWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFI


         IS6
hCavT1a  LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET
rCavT1a  LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET
hCavT2a  LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRARHLSNDSTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEP
hCavT3   LLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAKRRALGLYQALQSRRQ-----------
rCavT3   LLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAKRRALGLYQALQNRRQ-----------
```

Fig. 1A

```
hCavT1a QPSSSCCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQRDANGSRRLMLPPPSTPALSGAPPGA------ESVHSFYHADCHLEPVRC
rCavT1a QPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQRDANGSRRLMLPPPSTPTPSGGPPRGA------ESVHSFYHADCHLEPVRC
hCavT2a GHRQRRAGRHTASVHHLVYHHHHHHHHYHFSHGSPRRPGPEPGACDTRLVRAGAPPSPPSPGRGPPDAESVHSIYHADCHIEGPQERARVGTCRSHCRC
hCavT3  ------------------------------------------------------------------------------------------------
rCavT3  ------------------------------------------------------------------------------------------------

hCavT1a QAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLN-IPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSC
rCavT1a QAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFN-IPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSC
hCavT2a QPQAGHRAGHHELPHDPALRGGQRQHQPRTQGEVGRWTARHRGHGPLSLNSPDPYEKIPHVAGEHGLGQAPGHLSGLSVPCPLPSPPAGTLTCELKSC
hCavT3  -------ALGPEAPAPAKPGPHAKEPRHYQLCPQHSPLDATPHTLVQPIPATLASDPASC
rCavT3  -------AMGPGTPAPAKPGPHAKEPSHCKLCPRHSPLDPTPHTLVQPISAILASDPSSC

hCavT1a PYCARA-GAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS----------RR-QRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIM
rCavT1a PYCART-GAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHS----------RRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIM
hCavT2a PYCTRALEDPEGELSGSESGSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPSPQRRAQQRAAPGEPGWMGRLWVTFSGKLRRIVDSKYFSRGIM
hCavT3  PCCQHEDGRRPSGLGSTDSGQEGS------GSGSSAGGEDEADGDGARSSEDGASSELGKEEEEEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIM
rCavT3  PHCQHEAGRRPSGLGSTDSGQEGS------GSGGSA--EAEANGDGLQSSEDGVSSDLGKEEEQE---DGAARLCGDVWRETRKKLRGIVDSKYFNRGIM

         IIS1                                      IIS2                IIS3                   IIS4
hCavT1a IAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPA
rCavT1a IAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPA
hCavT2a MAILVNTLSMGVEYHEQPEELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIIVISVWEIVGQADGGLSVLRTFRLLRVLKLVRFLPA
hCavT3  MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPA
rCavT3  MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPA

         IIS5                                                            IIP LOOP
hCavT1a LQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMT
rCavT1a LQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMT
hCavT2a LRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLFGCKFSLKTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMT
hCavT3  LRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTPWASLYFVALMT
rCavT3  LRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTPWASLYFVALMT
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Fig. 1B

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         IIS6
hCavT1a  FGNYVLFENLLVAILVEGFQAEGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPL-----IIHTAATPMSLPKSTSTGLGEALGPASR
rCavT1a  FGNYVLFENLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPL-----IIHTAATPMSHPKSSSTGVGEALGSGSR
hCavT2a  FGNYVLFENLLVAILVEGFQAEGDANRSDTDEDKTSVHFEEDFHKLRELQTTELKMCSLAVTPNGTWRDEAACPLPSSCAQLPRPCLPPRAHHSWMQPPAS
hCavT3   FGNYVLFENLLVAILVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPKLCPIPMTPNGHLDPSLPLGGHLGPAGAAGPAPRLSLQPDPMIVAL
rCavT3   FGNYVLFENLLVAILVEGFQAEGDANRSCSDEDQSSSNLEEFDKLPEGLDNSRDLKLCPIPMTPNGHLDPSLPLGAHLGPAGTMGTAPRLSLQPDPVLVAL

hCavT1a  RTSSSGSAEPGAAH-EMKSPPSARSSPHSPWSAASSWTSRRSRSSRNSLGRAPSLKRR-----SPSGERRSLLSGEGQESQDEEESSEEERASP
rCavT1a  RTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSRSSRNSLGRAPSLKRR-----SPSGERRSLLSGEGQESQDEEESSEEDRASP
hCavT2a  QTLGVAAAAPGTRHWETRSLRQPPKFSLCPLGPSGAWSSRRSSWSSLGRAQPQA--------PACQCGERESLLSGEGKGSTDDEAEDGRARS
hCavT3   GSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWNSLKHKPPSAEHESLLSAERGGG-ARVCEVAADEGPPRAAPLHTPHAHIVHHGPHL
rCavT3   DSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWNSLKHKPPSAEHESLLSGEGGGSCVRACEGAREEAPTRTAPLHAPHAHHGPHL

hCavT1a  AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEH--QDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERD
rCavT1a  AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEH--QDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERD
hCavT2a  GPRATPLRRAESLDPR--------PLRRPPPAYQVRDRDGQVVALPSDFFLRIDSHREDAAELDDDSEDSCCLRLHKVLVPYKPQRCRSRRPG
hCavT3   AHRHRHRHRRTLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRMPSIAKDVFTKMGDRGDRGEDEEIDYTLCFRVRKMIDVYKPDWCEVRE
rCavT3   AHRHRHRHRRTLSLDTRDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFTKMDDRDRGEDEEIDYTLCFRVRKMIDVYKPDWCEVRE
                                                                                                   IIIS2
                   IIIS1
hCavT1a  SWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTKVVALGWCFGEQAYLRSSWNVLDGL
rCavT1a  SWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTKVVALGWCFGEQAYLRSSWNVLDGL
hCavT2a  PSTLYLFSPQNRFRVSCQKVITHKMFDHVVLVFIFLNCVTIALERPDIDPGSTERVFLSVSNYIFTAIFVAEMVKVVALGLLSGEHAYLQSSWNLLDGL
hCavT3   DWSVYLFSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGF
rCavT3   DWSVYLFSPENKFRILCQTIIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGF
                                                         IIIS4                        IIIS5
         IIIS3
hCavT1a  LVLISVIDILVSMVSDSGTKILGMIRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK
rCavT1a  LVLISVIDILVSMVSDSGTKILGMIRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK
hCavT2a  LVLVSLVDIVVAMASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFIIFGILGVQLFKGKFYYCEGPDTRNISTK
hCavT3   LVFVSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR
rCavT3   LVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR
```

Fig. 1C

IIIP LOOP   IIIS6
```
hCavT1a  SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEA
rCavT1a  SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEA
hCavT2a  AQCRAAHYRWVRRKYNFDNLGQALMSLFVLSSKDGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRPHQEAEEA
hCavT3   SDCMAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEEA
rCavT3   SDCVAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEEA
```

                                   IVS1   IVS2
```
hCavT1a  RRREEKRLRRLEKKRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLV
rCavT1a  RRREEKRLRRLEKKRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV
hCavT2a  RRREEKRLRRLERRRR-STFPSPEAQRRPYYADYSPTRRWIHSLCTSHYLDLFITFIICVNVITMSMEHYNQPKSLDEALKYCNVFTIVFFEAALKLV
hCavT3   RRREEKRLRRLEKKRR-K------AQRLPYYATYCHTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFTVLEAVLKLV
rCavT3   RRREEKRLRRLEKKRR-K------AQRLPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFTVLEAVLKLV
```

              IVS3   IVS4   IVS5
```
hCavT1a  AFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVE
rCavT1a  AFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLFFIFAALGVE
hCavT2a  AFGFRRFFKDRWNQLDLAIVLLSVMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVE
hCavT3   AFGLRRLFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLFFIYAALGVE
rCavT3   AFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLFFIYAALGVE
```

                         IVP LOOP   IVS6
```
hCavT1a  LFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQEST---CYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE
rCavT1a  LFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQEST---CYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE
hCavT2a  LFGRLECSEDNPCEGLSRHATFSNFGMAFLTLFRVSTGDNWNGIMKDTLRECSREDKHCLSYLPAPSPVYFVTFVLVPQFVLVNVVAVLMKHLEESNKE
hCavT3   LFGKLVCNDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVAVLMKHLDDSNKE
rCavT3   LFGKLVCNDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVSPLYFVSFVLTAQFVLINVVAVLMKHLDDSNKE
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hCavT1a  AKEEAELEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPKPGALHPAAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPND
rCavT1a  AKEEAELEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPKPGALHPAAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPND
hCavT2a  AREDAELDAEIELEMAQGPGSARRV------------------------------DADRPPLPQESPGARDAPNLVARKVSVSRMLSLPND
hCavT3   AQEDAEMDAEIELEMAHGLGP--------------------------------------------------
rCavT3   AQEDAEMDAEIELEMAHGLGPCPGPGPCPCPGPGPCPCPCPCA------------------------------------
```

Fig. 1D

```
hCaᵥT1a  SYMCRHGSTAEGPLGHRGWGLPLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRE
rCaᵥT1a  SYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRE
hCaᵥT2a  SYMFRPVVPASAPHPRPLQEVEMETYGAGTPLGSVASVHSPPAESCASLQIPLAVSSPARSGE-------------
hCaᵥT3   -----------GPRLPTGSPGAPGRGPGAGGGGDTDGGLCRRCYSPAQENLWLDSVSLIIKDS-------------
rCaᵥT3   -----------GPRLPTSSPGAPGRGSGGAGAGGDTESHLCRHCYSPAQETLWLDSVSLIIKDS-------------

hCaᵥT1a  DLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVE
rCaᵥT1a  DLLSEVSGPSPCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSS-QEEPLFPRDLKKCYSVE
hCaᵥT2a  -----------PLHALSPRGTARSPSLSRLLCRQEAVHTDSLKGRLTALGTPWILQSLVRKPR (SEQ ID NO:9)
hCaᵥT3   -----------LEGELTIIDNLSGSIFHHYSSPAGCKKCHHDKQETGPRPSCWVTT (SEQ ID NO:11)
rCaᵥT3   -----------LEGELTIIDNLSGSVFHHYASPDGCGKCHHDKQETGLHPSCWGMT (SEQ ID NO:12)

hCaᵥT1a  AQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPD
rCaᵥT1a  TQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLD

hCaᵥT1a  SMAASPSPKKDVLSLSGLSSDPADLDP (SEQ ID NO:1)
rCaᵥT1a  STAASPSPKKDTLSLSGLSSDPTDMDP (SEQ ID NO:5)
```

Fig. 1E
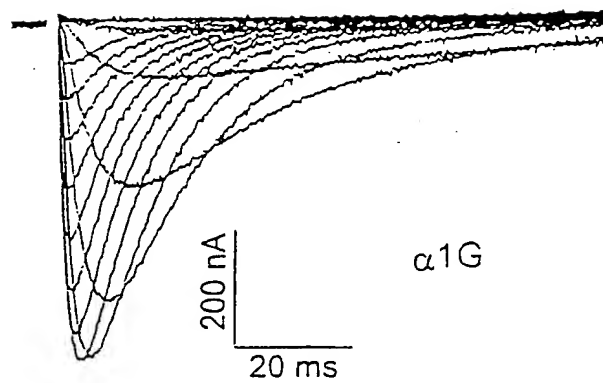
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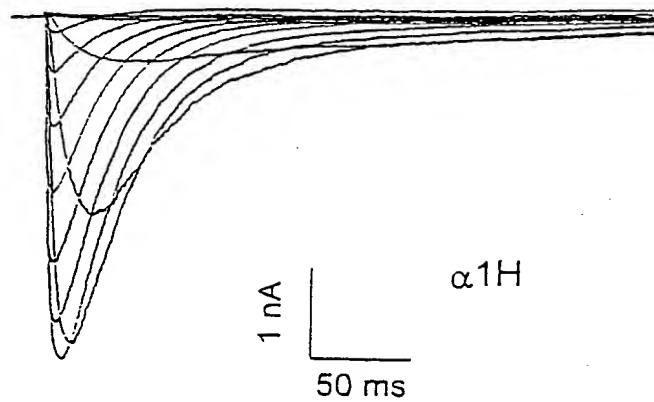
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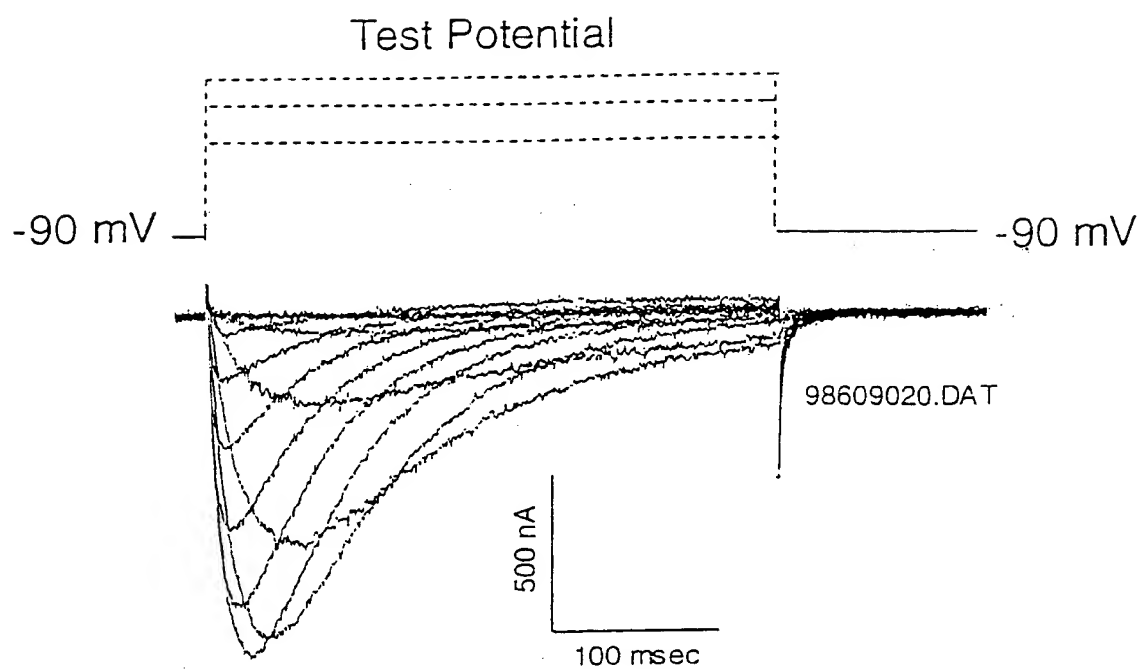
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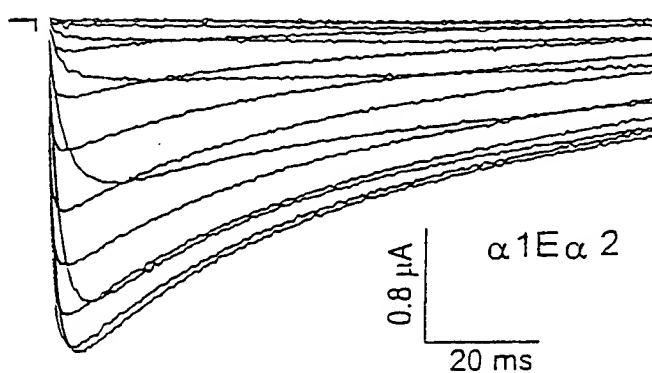
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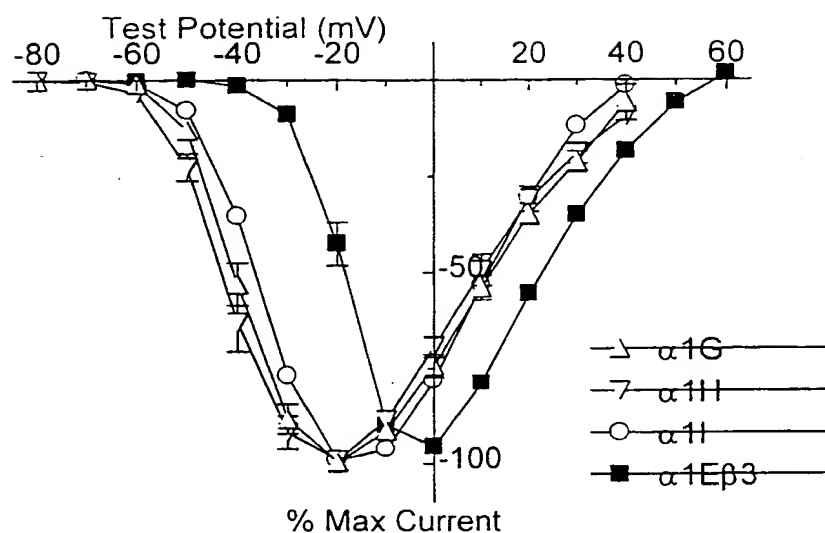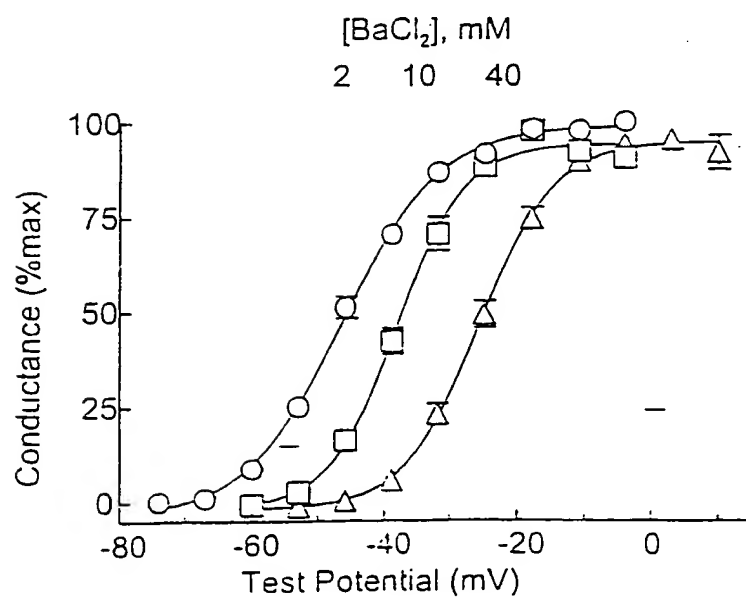
Figure 3A

Figure 3B
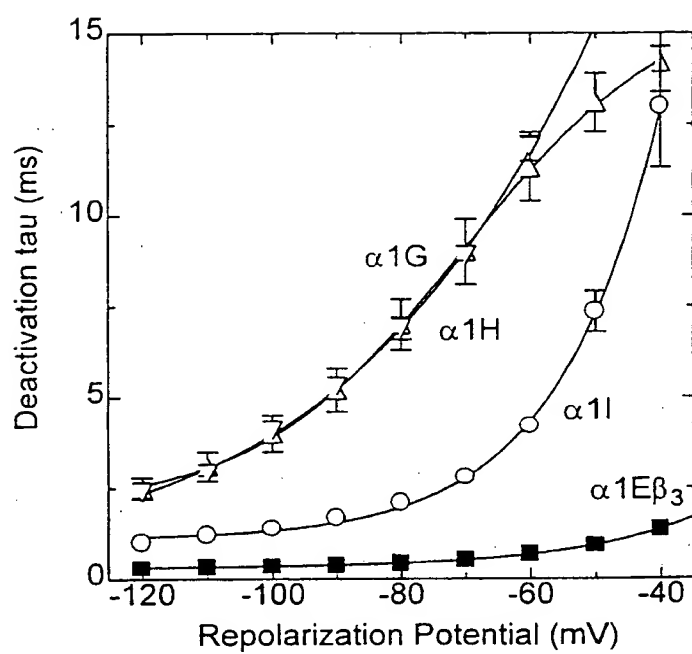
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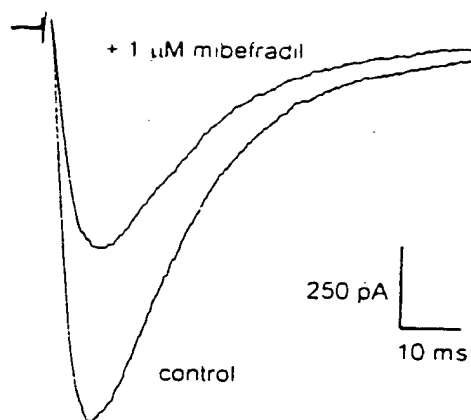
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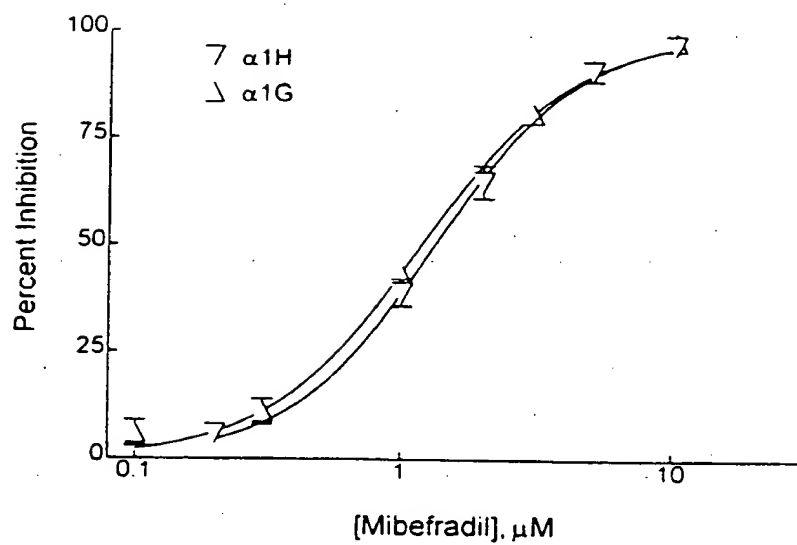
Figure 5B

SEQUENCE LISTING

<110> Perez-Reyes, Edward
      Cribbs, Leanne L.
      Loyola University of Chicago

<120> T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF
      USING SAME

<130> 89066

<140>
<141>

<150> US 08/985,809
<151> 1997-12-05

<160> 13

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg   96
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
                20   25   30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg   144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
            35   40   45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg   192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
        50   55   60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac   240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65   70   75   80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg   288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85   90   95

acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag   336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
                100   105   110

cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt   384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
            115   120   125

gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa   432

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        Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
            130             135             140

 5      aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc      480
        Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
        145             150             155             160

        atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc      528
10      Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                        165             170             175

        tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
        Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
15                      180             185             190

        cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg      624
        Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
                        195             200             205

20      ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc      672
        Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
            210             215             220

        ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga      720
25      Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
        225             230             235             240

        tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag      768
        Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
30                      245             250             255

        cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc      816
        Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
35                      260             265             270

        cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg      864
        Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
                        275             280             285

40      cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc      912
        Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
            290             295             300

        tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac      960
45      Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
        305             310             315             320

        acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac     1008
        Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
50                      325             330             335

        ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg     1056
        Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                        340             345             350

55      ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc     1104
        Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
                        355             360             365

60      ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc     1152
        Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
            370             375             380

        ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag     1200
```

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    Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
    385                 390             395             400

    acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc    1248
    Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                        405             410             415

    ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc    1296
    Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                    420             425             430

    tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc    1344
    Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
                435             440             445

    cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg    1392
    Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
            450             455             460

    ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc    1440
    Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
    465             470             475             480

    agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac    1488
    Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                    485             490             495

    cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc    1536
    His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
                    500             505             510

    agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg    1584
    Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
                515             520             525

    tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg    1632
    Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
            530             535             540

    gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac    1680
    Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
    545             550             555             560

    tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca    1728
    Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
                    565             570             575

    tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc    1776
    Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                580             585             590

    gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta    1824
    Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
                595             600             605

    gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc    1872
    Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
            610             615             620

    cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt    1920
    Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
    625             630             635             640

    aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa    1968
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                        645             650             655

 5      gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg   2016
        Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                        660             665             670

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10      Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
                        675             680             685

        gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac   2112
        Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
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        Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
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        Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
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        cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc   2256
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        gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc   2352
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35                      770             775             780

        ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt   2400
        Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
        785             790             795             800

40      ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc   2448
        Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                        805             810             815

        atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg   2496
45      Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
                        820             825             830

        ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg   2544
        Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
50                      835             840             845

        ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac   2592
        Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
55                      850             855             860

        gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc   2640
        Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
        865             870             875             880

60      atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat   2688
        Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                        885             890             895

        ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc   2736
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              Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
                       900                 905                 910

    5         atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc    2784
              Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
                       915                 920                 925

              ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc    2332
   10         Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
                       930                 935                 940

              att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc    2880
              Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
                  945                 950                 955                 960
   15
              gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc    2928
              Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                               965                 970                 975

   20         gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac    2976
              Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
                           980                 985                 990

              agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg    3024
   25         Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
                       995                 1000                1005

              cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc    3072
              Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
   30             1010                1015                1020

              atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc    3120
              Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
                  1025                1030                1035                1040
   35
              cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg    3168
              Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                           1045                1050                1055

   40         gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc    3216
              Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
                           1060                1065                1070

              ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac    3264
   45         Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
                       1075                1080                1085

              agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag    3312
   50         Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
                       1090                1095                1100

              cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag    3360
              Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
   55             1105                1110                1115                1120

              gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc    3408
              Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                           1125                1130                1135

   60         cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca    3456
              His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
                       1140                1145                1150

              gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg    3504
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             Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
                     1155                1160                1165

    5        tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc    3552
             Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
                     1170                1175                1180

             ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac    3600
   10        Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
                     1185                1190                1195                1200

             gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg     3648
             Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                     1205                1210                1215
   15
             atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca    3696
             Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
                         1220                1225                1230

   20        gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg    3744
             Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
                     1235                1240                1245

             atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc    3792
   25        Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
                     1250                1255                1260

             ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac    3840
   30        Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
                     1265                1270                1275                1280

             agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca    3888
             Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                         1285                1290                1295
   35
             gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc    3936
             Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
                         1300                1305                1310

   40        ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg    3984
             Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
                     1315                1320                1325

             ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct    4032
   45        Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
                     1330                1335                1340

             gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg    4080
   50        Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
                     1345                1350                1355                1360

             cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag    4128
             Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                         1365                1370                1375
   55
             ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att    4176
             Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
                     1380                1385                1390

   60        gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg    4224
             Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
                     1395                1400                1405

             cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg    4272
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        Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
           1410              1415                1420

    aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc      4320
 5  Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
       1425              1430                1435                1440

    cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg      4368
10  Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                      1445                1450                1455

    ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg      4416
    Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
15           1460                1465                1470

    ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc      4464
    Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
             1475                1480                1485

20  tgg atg ctg ctg tac ttc atc tcg ttc ctc att gtg gcc ttc ttt         4512
    Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
       1490              1495                1500

    gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt      4560
25  Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
    1505              1510                1515                1520

    cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc      4608
    Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
30                    1525                1530                1535

    cta cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct      4656
    Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
35           1540                1545                1550

    gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc cgg ctc      4704
    Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu
             1555                1560                1565

40  ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc atc aca      4752
    Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr
       1570              1575                1580

    ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac tac cag      4800
45  Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln
    1585              1590                1595                1600

    cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac atc ttc      4848
    Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe
50                    1605                1610                1615

    act gtc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt      4896
    Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly
55           1620                1625                1630

    ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg gcc att      4944
    Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile
             1635                1640                1645

60  gtg ctg ctg tcc atc atg ggc atc acg ctg gag gaa atc gag gtc aac      4992
    Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn
       1650              1655                1660

    gcc tcg ctg ccc atc aac ccc acc atc atc cgc atc atg agg gtg ctg      5040
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      Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu
      1665                1670                1675                1680

 5    cgc att gcc cga gtg ctg aag ctg ctg aag atg gct gtg ggc atg cgg   5088
      Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg
                          1685                1690                1695

      gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg   5136
      Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu
10                        1700                1705                1710

      gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gct ctg ggc gtg   5184
      Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val
15            1715                1720                1725

      gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt gag ggc   5232
      Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly
          1730                1735                1740

20    ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc cta acc   5280
      Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr
      1745                1750                1755                1760

      ctc ttc cga gtc tcc aca ggt gac aat tgg aat ggc att atg aag gac   5328
25    Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp
                          1765                1770                1775

      acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg gtc atc   5376
      Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile
30                        1780                1785                1790

      tcg cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttc gtg cta   5424
      Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu
              1795                1800                1805
35
      gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag agc aac   5472
      Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn
          1810                1815                1820

40    aag gag gcc aag gag gag gcc gag cta gag gct gag ctg gag ctg gag   5520
      Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu
      1825                1830                1835                1840

      atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc ccc ttc   5568
45    Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe
                          1845                1850                1855

      ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc aag cct   5616
      Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro
50                        1860                1865                1870

      ggg gct ctg cac cca gcg gcc cac gcg aga tca gcc tcc cac ttt tcc   5664
      Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His Phe Ser
              1875                1880                1885
55
      ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca gga cca   5712
      Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro
          1890                1895                1900

60    gac tta ctg act gtg cgg aag tct ggg gtc agc cga acg cac tct ctg   5760
      Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
      1905                1910                1915                1920

      ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag ggg ccc   5808
```

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        Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro
                1925                    1930               Thr Ala Glu Gly Pro
                                                                1935

  5     ctg gga cac agg ggc tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc    5556
        Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val
                1940                    1945               1950

        ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg cag ctt    5904
        Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu
 10             1955                    1960               1965

        ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca acc tgg    5952
        Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro Thr Trp
                1970                    1975               1980
 15
        ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg gct cag    6000
        Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
        1985                1990               1995               2000

 20     agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg gac gtt    6048
        Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
                2005                    2010               2015

 25     cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt ggg ccc    6096
        Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro
                2020                    2025               2030

        tcc ccg ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca agt acc    6144
        Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr
 30             2035                    2040               2045

        cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag cac atg    6192
        Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys His Met
                2050                    2055               2060
 35
        acc ccg cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc aag ggc    6240
        Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly
        2065                2070               2075               2080

 40     cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg agc tgg    6288
        Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
                2085                    2090               2095

 45     att tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc cca tcc    6336
        Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser
                2100                    2105               2110

        cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc tgc cag    6384
        Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln
 50             2115                    2120               2125

        cgc cgg cct acg tcc tgg ctg gat gag cag agg aga cac tct atc gcc    6432
        Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala
                2130                    2135               2140
 55
        gtc agc tgc ctg gac agc ggc tcc caa ccc cac ctg ggc aca gac ccc    6480
        Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro
        2145                2150               2155               2160

 60     tct aac ctt ggg ggc cag cct ctt ggg ggg cct ggg agc cgg ccc aag    6528
        Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys
                2165                    2170               2175

        aaa aaa ctc agc ccg cct agt atc acc ata gac ccc ccc gag agc caa    6576
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     Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln
               2180                2185                2190

 5   ggt cct cgg acc ccg ccc agc cct ggt atc tgc ctc cgg agg agg gct    6624
     Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala
               2195                2200                2205

     ccg tcc agc gac tcc aag gat ccc ttg gcc tct ggc ccc cct gac agc    6672
     Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser
10             2210                2215                2220

     atg gct gcc tcg ccc tcc cca aag aaa gat gtg ctg agt ctc tcc ggt    6720
     Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly
     2225                2230                2235                2240
15

     tta tcc tct gac cca gca gac ctg gac ccc                            6750
     Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
                         2245                2250

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     Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
     1               5                  10                  15
35
     cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg    96
     Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
                     20                  25                  30

     ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg    144
40   Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
                 35                  40                  45

     gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg    192
     Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
45               50                  55                  60

     agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac    240
     Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
     65                  70                  75                  80
50
     ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg    288
     Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                     85                  90                  95
55
     acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag    336
     Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
                     100                 105                 110

     cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt    384
60   Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
                 115                 120                 125

     gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa    432
     Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
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                130                     135                     140

      aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc   480
 5    Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
      145                     150                     155                160

      atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc   528
10    Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                          165                     170                     175

      tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac   576
      Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
                          180                     185                     190

15    cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg   624
      Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
                    195                     200                     205

      ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc   672
20    Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
                210                     215                     220

      ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga   720
25    Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
      225                     230                     235                240

      tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag   768
      Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
30                        245                     250                     255

      cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc   816
      Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                    260                     265                     270

35    cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg   864
      Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
                275                     280                     285

      cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc   912
40    Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
                290                     295                     300

      tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac   960
      Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
45    305                     310                     315                320

      acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac  1008
      Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                    325                     330                     335

50    ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg  1056
      Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                340                     345                     350

55    ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc  1104
      Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
                355                     360                     365

      ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc  1152
60    Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
                370                     375                     380

      ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag  1200
      Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
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          385                    390                    395                    400
     acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc   1248
 5   Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                         405                    410                    415

     ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc   1296
10   Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                         420                    425                    430

     tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc   1344
     Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
                     435                    440                    445

15   cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg   1392
     Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
                 450                    455                    460

     ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc   1440
20   Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
     465                    470                    475                    480

     agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac   1488
     Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
25                   485                    490                    495

     cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc   1536
     His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
30                   500                    505                    510

     agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg   1584
     Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
                 515                    520                    525

35   tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg   1632
     Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
                 530                    535                    540

     gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac   1680
40   Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
     545                    550                    555                    560

     tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca   1728
     Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
45                   565                    570                    575

     tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc   1776
     Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                 580                    585                    590

50
     gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta   1824
     Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
                 595                    600                    605

55   gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc   1872
     Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
                 610                    615                    620

     cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt   1920
60   Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
     625                    630                    635                    640

     aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa   1968
     Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
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                 645                        650                        655

    gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg    2016
    Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
5               660                  665                  670

    gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca    2064
    Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
10              675                  680                  685

    gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac    2112
    Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
                690                  695                  700

15  ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca    2160
    Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
    705                  710                  715                  720

    gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc    2208
20  Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                     725                  730                  735

    cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc    2256
    Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
25                   740                  745                  750

    atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc    2304
    Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
                     755                  760                  765
30
    gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc    2352
    Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    770                  775                  780

35  ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt    2400
    Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
    785                  790                  795                  800

    ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc    2448
40  Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                     805                  810                  815

    atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg    2496
    Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
45                   820                  825                  830

    ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg    2544
    Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
                     835                  840                  845
50
    ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac    2592
    Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    850                  855                  860

55  gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc    2640
    Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
    865                  870                  875                  880

    atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat    2688
60  Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                     885                  890                  895

    ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc    2736
    Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
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                    900                    905                    910

      atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc   2784
 5    Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
              915                    920                    925

      ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc   2832
      Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
10            930                    935                    940

      att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc   2880
      Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
      945                    950                    955                    960

15    gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc   2928
      Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                     965                    970                    975

      gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac   2976
20    Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
                     980                    985                    990

      agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg   3024
      Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
25            995                    1000                   1005

      cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc   3072
      Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
30            1010                   1015                   1020

      atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc   3120
      Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
      1025                   1030                   1035                   1040

35    cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg   3168
      Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                     1045                   1050                   1055

      gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc   3216
40    Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
                     1060                   1065                   1070

      ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac   3264
      Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
45            1075                   1080                   1085

      agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag   3312
      Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
50            1090                   1095                   1100

      cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag   3360
      Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
      1105                   1110                   1115                   1120

55    gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc   3408
      Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                     1125                   1130                   1135

      cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca   3456
60    His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
                     1140                   1145                   1150

      gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg   3504
      Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
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                 1155                    1160                    1165
       tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc    3552
       Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
  5       1170                1175                1180

       ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac    3600
       Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
       1185                1190                1195                1200
 10
       gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg    3648
       Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                  1205                1210                1215

 15    atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca    3696
       Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
                  1220                1225                1230

       gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg    3744
 20    Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
              1235                1240                1245

       atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc    3792
       Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
 25       1250                1255                1260

       ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac    3840
       Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
       1265                1270                1275                1280
 30
       agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca    3888
       Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                  1285                1290                1295

 35    gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc    3936
       Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
              1300                1305                1310

       ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg    3984
 40    Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
              1315                1320                1325

       ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct    4032
       Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
 45       1330                1335                1340

       gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg    4080
       Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
       1345                1350                1355                1360
 50
       cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag    4128
       Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                  1365                1370                1375

 55    ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att    4176
       Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
                  1380                1385                1390

       gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg    4224
 60    Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
              1395                1400                1405

       cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg    4272
       Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
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              1410                    1415                   1420

 5    aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc    4320
      Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
      1425                1430                1435                1440


      cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg    4368
      Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                          1445                1450                1455
10

      ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg    4416
      Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
                  1460                1465                1470

15    ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc    4464
      Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
                  1475                1480                1485


      tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt    4512
20    Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
                  1490                1495                1500


      gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt    4560
25    Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
      1505                1510                1515                1520


      cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc    4608
      Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                          1525                1530                1535
30

      cta cga aga ctg gag aaa aag aga agg aat cta atg ctg gac gat gta    4656
      Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp Asp Val
                  1540                1545                1550

35    att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag tgc aaa    4704
      Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln Cys Lys
                  1555                1560                1565


      cct tac tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg    4752
40    Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
                  1570                1575                1580


      tgc acc agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg    4800
      Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
45    1585                1590                1595                1600


      aac gtg gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg    4848
      Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
                  1605                1610                1615
50

      gat gag gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc    4896
      Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
                  1620                1625                1630

55    ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc    4944
      Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
                  1635                1640                1645


      cag gac agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc    4992
60    Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
                  1650                1655                1660


      atg ggc atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc    5040
      Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile
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         1665                1670              1675              1680

      aac ccc acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg    5088
      Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val
  5                1685              1690              1695

      ctg aag ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg    5136
      Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr
 10                1700              1705              1710

      gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg    5184
      Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met
 15                1715              1720              1725

      ttg ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac    5232
      Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp
 20                1730              1735              1740

      ctg gag tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc    5280
      Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
 25       1745              1750              1755              1760

      acc ttt cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc    5328
      Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser
 30                1765              1770              1775

      aca ggt gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt    5376
      Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys
 35                1780              1785              1790

      gac cag gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt    5424
      Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
 40                1795              1800              1805

      gtg tcc ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc    5472
      Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
 45                1810              1815              1820

      gcc gtg ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag    5520
      Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
 50       1825              1830              1835              1840

      gag gcc gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc    5568
      Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
                  1845              1850              1855

      ccc cag ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc    5616
      Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
                  1860              1865              1870

      gag ggc ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca    5664
      Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro
                  1875              1880              1885

      gcg gcc cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg    5712
      Ala Ala His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr
                  1890              1895              1900

      atg cag ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg    5760
      Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val
                  1905              1910              1915              1920

      cgg aag tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac    5808
      Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr
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                1925                  1930                  1935

     atg tgt cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc      5856
     Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly
             1940              1945              1950

     tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc      5904
     Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser
             1955              1960              1965

     cag cca gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct      5952
     Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro
          1970              1975              1980

     cat ctg ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa      6000
     His Leu Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys
     1985              1990              1995              2000

     ctg ccc cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc      6048
     Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg
                   2005              2010              2015

     cag gca gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc      6096
     Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser
                   2020              2025              2030

     cgg gaa gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc      6144
     Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala
             2035              2040              2045

     cgg gcc tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac      6192
     Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His
          2050              2055              2060

     tcc cgc agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct      6240
     Ser Arg Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro
     2065              2070              2075              2080

     tgc cca ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga      6288
     Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg
                   2085              2090              2095

     agc agc tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc      6336
     Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu
                   2100              2105              2110

     ctg ccc cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag      6384
     Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys
             2115              2120              2125

     aag tgc tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc      6432
     Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser
          2130              2135              2140

     tgg ctg gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac      6480
     Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp
     2145              2150              2155              2160

     agc ggc tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc      6528
     Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly
                   2165              2170              2175

     cag cct ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg      6576
     Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro
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                    2180                  2185                   2190

      cct agt atc acc ata gac ccc ccc gag agc caa ggt cct cgg acc ccg    6624
      Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro
5                   2195                  2200                   2205

      ccc agc cct ggt atc tgc ctc cgg agg agg gct ccg tcc agc gac tcc    6672
      Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser
10                  2210                  2215                   2220

      aag gat ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc    6720
      Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro
      2225                  2230                  2235                   2240

15    tcc cca aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca    6768
      Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro
                    2245                  2250                   2255

      gca gac ctg gac ccc                                                6783
20    Ala Asp Leu Asp Pro
                    2260


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      atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc    48
35    Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
      1                   5                    10                     15

      cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg    96
      Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
40                  20                   25                     30

      ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg    144
      Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
                    35                   40                   45
45
      gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg    192
      Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
          50                   55                   60

50    agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac    240
      Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
      65                   70                   75                     80

      ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg    288
55    Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                    85                   90                     95

      acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag    336
      Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
60                  100                  105                    110

      cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttc    384
      Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
          115                  120                    125
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gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa    432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130             135             140

aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc    480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145             150             155             160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc    528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
            165             170             175

tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180             185             190

cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg    624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
            195             200             205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc    672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210             215             220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga    720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225             230             235             240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag    768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
            245             250             255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc    816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260             265             270

cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg    864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
            275             280             285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc    912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290             295             300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac    960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305             310             315             320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac    1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
            325             330             335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg    1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340             345             350

ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc    1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
            355             360             365

ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc    1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370             375             380
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ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag      1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc      1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc      1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                420                 425                 430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc      1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
                435                 440                 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg      1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
        450                 455                 460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc      1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465                 470                 475                 480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac      1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc      1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
                500                 505                 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg      1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
                515                 520                 525

tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg      1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
        530                 535                 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac      1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca      1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
                565                 570                 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc      1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                580                 585                 590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta      1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
                595                 600                 605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc      1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
        610                 615                 620

cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt      1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640
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      aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa    1963
  5   Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
                        645                 650                 655

      gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg    2016
      Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                        660                 665                 670

 10   gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca    2064
      Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
                        675                 680                 685

      gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac    2112
 15   Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
                        690                 695                 700

      ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca    2160
 20   Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
      705                 710                 715                 720

      gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc    2208
      Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                        725                 730                 735
 25

      cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc    2256
      Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
                        740                 745                 750

 30   atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc    2304
      Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
                        755                 760                 765

      gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc    2352
 35   Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
      770                 775                 780

      ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt    2400
      Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
 40   785                 790                 795                 800

      ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc    2448
      Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                        805                 810                 815
 45

      atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg    2496
      Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
                        820                 825                 830

 50   ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg    2544
      Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
                        835                 840                 845

      ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac    2592
 55   Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
      850                 855                 860

      gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc    2640
      Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
 60   865                 870                 875                 880

      atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat    2688
      Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                        885                 890                 895
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ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc   2736
Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
            900             905             910

atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc   2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
            915             920             925

ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc   2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
            930             935             940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc   2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945             950             955             960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc   2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
            965             970             975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac   2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980             985             990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg   3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
            995             1000            1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc   3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
            1010            1015            1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc   3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025            1030            1035            1040

cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg   3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
            1045            1050            1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc   3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060            1065            1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac   3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
            1075            1080            1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag   3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
            1090            1095            1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag   3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105            1110            1115            1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc   3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
            1125            1130            1135

cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca   3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140            1145            1150
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     gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg   3504
     Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
             1155                1160                1165

     tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc   3552
     Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
         1170                1175                1180

     ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac   3600
     Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
     1185                1190                1195                1200

     gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg   3648
     Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
             1205                1210                1215

     atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca   3696
     Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
             1220                1225                1230

     gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg   3744
     Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
             1235                1240                1245

     atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc   3792
     Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
         1250                1255                1260

     ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac   3840
     Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
     1265                1270                1275                1280

     agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca   3888
     Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
             1285                1290                1295

     gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc   3936
     Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
             1300                1305                1310

     ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg   3984
     Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
             1315                1320                1325

     ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct   4032
     Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
         1330                1335                1340

     gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg   4080
     Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
     1345                1350                1355                1360

     cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag   4128
     Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
             1365                1370                1375

     ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att   4176
     Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
             1380                1385                1390

     gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg   4224
     Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
             1395                1400                1405
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cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg    4272
Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
    1410              1415              1420

aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc    4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425              1430              1435              1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg    4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
             1445              1450              1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg    4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
         1460              1465              1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc    4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
         1475              1480              1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt    4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
     1490              1495              1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt    4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505              1510              1515              1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc    4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
             1525              1530              1535

cta cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct    4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
         1540              1545              1550

gat cta atg ctg gac gat gta att gct tcc ggc agc tca gcc agc gct    4704
Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala
         1555              1560              1565

gcg tca gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc    4752
Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
         1570              1575              1580

cgg ctc ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc    4800
Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
1585              1590              1595              1600

atc aca ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac    4848
Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
             1605              1610              1615

tac cag cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac    4896
Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
         1620              1625              1630

atc ttc act gtc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc    4944
Ile Phe Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala
         1635              1640              1645

ttt ggt ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg    4992
Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
         1650              1655              1660
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gcc att gtg ctg ctg tcc atc atg ggc atc acg ctg gag gaa atc gag    5040
Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu
1665            1670            1675            1680

gtc aac gcc tcg ctg ccc atc aac ccc acc atc atc cgc atc atg agg    5088
Val Asn Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
                1685            1690            1695

gtg ctg cgc att gcc cga gtg ctg aag ctg ctg aag atg gct gtg ggc    5136
Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
        1700            1705            1710

atg cgg gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg    5184
Met Arg Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly
        1715            1720            1725

aac ctg gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gct ctg    5232
Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
    1730            1735            1740

ggc gtg gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt    5280
Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
1745            1750            1755            1760

gag ggc ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc    5328
Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
                1765            1770            1775

cta acc ctc ttc cga gtc tcc aca ggt gac aat tgg aat ggc att atg    5376
Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
        1780            1785            1790

aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg    5424
Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
        1795            1800            1805

gtc atc tcg cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttc    5472
Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
    1810            1815            1820

gtg cta gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag    5520
Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
1825            1830            1835            1840

agc aac aag gag gcc aag gag gag gcc gag cta gag gct gag ctg gag    5568
Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu
                1845            1850            1855

ctg gag atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc    5616
Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
        1860            1865            1870

ccc ttc ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc    5664
Pro Phe Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro
        1875            1880            1885

aag cct ggg gct ctg cac cca gcg gcc cac gcg aga tca gcc tcc cac    5712
Lys Pro Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His
    1890            1895            1900

ttt tcc ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca    5760
Phe Ser Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro
1905            1910            1915            1920
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5        gga cca gac tta ctg act gtg cgg aag tct ggg gtc agc cga acg cac    5808
         Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His
                          1925                1930                1935

         tct ctg ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag    5856
         Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu
                          1940                1945                1950

10       ggg ccc ctg gga cac agg ggc tgg ggg ctc ccc aaa gct cag tca ggc    5904
         Gly Pro Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly
                      1955                1960                1965

         tcc gtc ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg    5952
15       Ser Val Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu
                  1970                1975                1980

         cag ctt ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca    6000
         Gln Leu Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro
20       1985                1990                1995                2000

         acc tgg ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg    6048
         Thr Trp Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu
                          2005                2010                2015
25
         gct cag agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg    6096
         Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu
                      2020                2025                2030

30       gac gtt cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt    6144
         Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser
                  2035                2040                2045

         ggg ccc tcc ccg ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca    6192
35       Gly Pro Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser
              2050                2055                2060

         agt acc cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag    6240
         Ser Thr Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys
40       2065                2070                2075                2080

         cac atg acc ccg cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc    6288
         His Met Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly
                          2085                2090                2095
45
         aag ggc cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg    6336
         Lys Gly Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu
                      2100                2105                2110

50       agc tgg att tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc    6384
         Ser Trp Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro
                  2115                2120                2125

         cca tcc cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc    6432
55       Pro Ser Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser
              2130                2135                2140

         tgc cag cgc cgg cct acg tcc tgg ctg gat gag cag agg aga cac tct    6480
         Cys Gln Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser
60       2145                2150                2155                2160

         atc gcc gtc agc tgc ctg gac agc ggc tcc caa ccc cac ctg ggc aca    6528
         Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr
                      2165                2170                2175
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gac ccc tct aac ctt ggg ggc cag cct ctc ggg ggg cct ggg agc cgg        6576
Asp Pro Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg
            2180                2185                2190

ccc aag aaa aaa ctc agc ccg cct agt atc acc ata gac ccc ccc gag        6624
Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu
        2195                2200                2205

agc caa ggt cct cgg acc ccg ccc agc cct ggt atc tgc ctc cgg agg       6672
Ser Gln Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg
        2210                2215                2220

agg gct ccg tcc agc gac tcc aag gat ccc ttg gcc tct ggc ccc cct       6720
Arg Ala Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro
2225                2230                2235                2240

gac agc atg gct gcc tcg ccc tcc cca aag aaa gat gtg ctg agt ctc       6768
Asp Ser Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu
            2245                2250                2255

tcc ggt tta tcc tct gac cca gca gac ctg gac ccc                        6804
Ser Gly Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
        2260                2265


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atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc         48
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
1                   5                   10                  15

cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg         96
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg        144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg        192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
        50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac        240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg        288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
            85                  90                  95

acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag        336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
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cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt      384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115             120             125

gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
        130             135             140

aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc      480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145             150             155             160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165             170             175

tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180             185             190

cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
            195             200             205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
            210             215             220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225             230             235             240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245             250             255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc      816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                260             265             270

cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
            275             280             285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc      912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
            290             295             300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305             310             315             320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325             330             335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340             345             350

ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc     1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
            355             360             365
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ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc    1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370             375             380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag    1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385             390             395             400

acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc    1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405             410             415

ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc    1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420             425             430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc    1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435             440             445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggc ctg    1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
    450             455             460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc    1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465             470             475             480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac    1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
            485             490             495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc    1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
        500             505             510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg    1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515             520             525

tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg    1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
    530             535             540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac    1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545             550             555             560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca    1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
            565             570             575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc    1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580             585             590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta    1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
        595             600             605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc    1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610             615             620
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cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt    1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa    1968
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
                    645                 650                 655

gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg    2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                660                 665                 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca    2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
            675                 680                 685

gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac    2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
        690                 695                 700

ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca    2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705                 710                 715                 720

gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc    2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                    725                 730                 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc    2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
                740                 745                 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc    2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
            755                 760                 765

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc    2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
        770                 775                 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt    2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785                 790                 795                 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc    2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                    805                 810                 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg    2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
                820                 825                 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg    2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
            835                 840                 845

ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac    2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
        850                 855                 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc    2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865                 870                 875                 880
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        atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat      2688
   5    ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc      2736
  10    atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc      2784
  15    ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc      2832
  20    att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc      2880
        gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc      2928
  25    gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac      2976
  30    agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg      3024
  35    cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc      3072
  40    atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc      3120
        cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg      3168
  45    gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc      3216
  50    ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac      3264
  55    agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag      3312
  60    cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag      3360
        gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc      3408
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  5     Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                       885                390                    895

        Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
                       900                905                    910

        Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
                       915                920                    925

        Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
                       930                935                    940

        Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
        945                950                955                    960

        Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                       965                970                    975

        Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
                       980                985                    990

        Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
                       995                1000               1005

        Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
           1010               1015                  1020

        Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
        1025               1030               1035                  1040

        Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                       1045               1050               1055

        Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
                       1060               1065                  1070

        Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
                       1075               1080               1085

        Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
           1090               1095               1100

        Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
        1105               1110               1115                  1120

        Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                       1125               1130                  1135
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cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca    3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                    1145                    1150

gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg    3504
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
            1155                    1160                    1165

tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc    3552
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
            1170                    1175                    1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac    3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
     1185               1190                    1195               1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg    3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
            1205                    1210                    1215

atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca    3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
            1220                    1225                    1230

gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg    3744
Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
            1235                    1240                    1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc    3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
            1250                    1255                    1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac    3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
     1265               1270                    1275               1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca    3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
            1285                    1290                    1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc    3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
            1300                    1305                    1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg    3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
            1315                    1320                    1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct    4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
            1330                    1335                    1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg    4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
     1345               1350                    1355               1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag    4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
            1365                    1370                    1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att    4176
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
            1380                    1385                    1390
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         gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg   4224
         Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
             1395                1400                1405

  5      cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg   4272
         Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
             1410                1415                1420

 10      aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc   4320
         Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
         1425                1430                1435                1440

         cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg   4368
         Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
 15                          1445                1450                1455

         ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg   4416
         Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
                     1460                1465                1470
 20
         ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc   4464
         Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
                 1475                1480                1485

 25      tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt   4512
         Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
                 1490                1495                1500

         gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt   4560
 30      Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
         1505                1510                1515                1520

         cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc   4608
         Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
 35                          1525                1530                1535

         cta cga aga ctg gag aaa aag aga agg aaa gcc cag tgc aaa cct tac   4656
         Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys Pro Tyr
                     1540                1545                1550
 40
         tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg tgc acc   4704
         Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu Cys Thr
                 1555                1560                1565

 45      agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg aac gtg   4752
         Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val
             1570                1575                1580

         gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg gat gag   4800
 50      Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu
         1585                1590                1595                1600

         gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc ttg gag   4848
         Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val Leu Glu
 55                          1605                1610                1615

         tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc cag gac   4896
         Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp
                     1620                1625                1630
 60
         agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc atg ggc   4944
         Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly
             1635                1640                1645
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atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc aac ccc    4992
Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile Asn Pro
    1650               1655              1660

acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg ctg aag    5040
Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys
1665              1670              1675              1680

ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg gtg atg    5088
Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr Val Met
                 1685              1690              1695

cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg ttg ttg    5136
Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu
                 1700              1705              1710

ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac ctg gag    5184
Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu
        1715              1720              1725

tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc acc ttt    5232
Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe
    1730              1735              1740

cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc aca ggt    5280
Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly
1745              1750              1755              1760

gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt gac cag    5328
Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln
                 1765              1770              1775

gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt gtg tcc    5376
Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser
                 1780              1785              1790

ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc gcc gtg    5424
Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile Ala Val
        1795              1800              1805

ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag gag gcc    5472
Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala
    1810              1815              1820

gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc ccc cag    5520
Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln
1825              1830              1835              1840

ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc gag ggc    5568
Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly
                 1845              1850              1855

ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca gcg gcc    5616
Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro Ala Ala
                 1860              1865              1870

cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg atg cag    5664
His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr Met Gln
    1875              1880              1885

ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg cgg aag    5712
Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val Arg Lys
    1890              1895              1900
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tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac atg tgt     5760
Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys
1905                1910                1915                1920

cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc tgg ggg     5808
Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly Trp Gly
                    1925                1930                1935

ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc cag cca     5856
Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser Gln Pro
            1940                1945                1950

gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct cat ctg     5904
Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro His Leu
        1955                1960                1965

ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa ctg ccc     5952
Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys Leu Pro
        1970                1975                1980

cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc cag gca     6000
Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala
1985                1990                1995                2000

gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc cgg gaa     6048
Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu
                2005                2010                2015

gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc cgg gcc     6096
Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala Arg Ala
            2020                2025                2030

tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac tcc cgc     6144
Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His Ser Arg
        2035                2040                2045

agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct tgc cca     6192
Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro Cys Pro
        2050                2055                2060

ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga agc agc     6240
Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg Ser Ser
2065                2070                2075                2080

tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc ctg ccc     6288
Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro
                2085                2090                2095

cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag aag tgc     6336
Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys Lys Cys
            2100                2105                2110

tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc tgg ctg     6384
Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser Trp Leu
        2115                2120                2125

gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac agc ggc     6432
Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly
        2130                2135                2140

tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc agc cct     6480
Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly Gln Pro
2145                2150                2155                2160
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ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg cct agt    6528
Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser
             2165                 2170                 2175

atc acc ata gac ccc ccc gag agc caa ggt cct cgg acc ccg ccc agc    6576
Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro Pro Ser
             2180                 2185                 2190

cct ggt atc tgc ctc cgg agg agg gct ccg tcc agc gac tcc aag gat    6624
Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser Lys Asp
         2195                 2200                 2205

ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc tcc cca    6672
Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro Ser Pro
     2210                 2215                 2220

aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca gca gac    6720
Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Ala Asp
2225                 2230                 2235                 2240

ctg gac ccc                                                         6729
Leu Asp Pro


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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
 1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag     96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
             20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg    144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
         35                  40                  45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg    192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
     50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac    240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg    288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                 85                  90                  95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag    336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
             100                 105                 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt    384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
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                115                    120                    125

     gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag    432
     Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
5        130                    135                    140

     aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc    480
     Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
     145             150                    155                    160
10
     att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc    528
     Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                         165                    170                    175

15   tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
     Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
                         180                    185                    190

     cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg    624
20   Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
                     195                    200                    205

     cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc    672
     Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
25           210                    215                    220

     ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg    720
     Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
     225                    230                    235                    240
30
     tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag    768
     Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                         245                    250                    255

35   cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct    816
     Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                     260                    265                    270

     cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg    864
40   Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
                     275                    280                    285

     cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc    912
     Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
45           290                    295                    300

     tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat    960
     Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
     305                    310                    315                    320
50
     acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac    1008
     Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                         325                    330                    335

55   ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca    1056
     Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                     340                    345                    350

     ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc    1104
60   Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
                     355                    360                    365

     ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc    1152
     Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
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            370                    375                    380

      ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag   1200
      Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
 5    385                    390                    395                    400

      acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc   1248
      Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                           405                    410                    415
10
      ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc   1296
      Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                           420                    425                    430

15    tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc   1344
      Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
                           435                    440                    445

      cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg   1392
20    Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
                           450                    455                    460

      ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc   1440
      Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
25    465                    470                    475                    480

      agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac   1488
      Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                           485                    490                    495
30
      cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc   1536
      His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
                           500                    505                    510

35    aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg   1584
      Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
                           515                    520                    525

      tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg   1632
40    Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
                           530                    535                    540

      ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac   1680
      Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
45    545                    550                    555                    560

      tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca   1728
      Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                           565                    570                    575
50
      tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act   1776
      Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                           580                    585                    590

55    gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg   1824
      Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
                           595                    600                    605

      gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc   1872
60    Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
                           610                    615                    620

      cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt   1920
      Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
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         625                    630                    635                    640

     acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag   1963
 5   Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                     645                    650                    655

     gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg   2016
10   Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                     660                    665                    670

     aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca   2064
     Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
                     675                    680                    685

15   gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac   2112
     Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
                     690                    695                    700

     ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat   2160
20   Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
     705                    710                    715                    720

     gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca   2208
25   Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                     725                    730                    735

     ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc   2256
     Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
                     740                    745                    750
30
     gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag   2304
     Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
                     755                    760                    765

35   ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc   2352
     Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
                     770                    775                    780

     agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc   2400
40   Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
     785                    790                    795                    800

     ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg   2448
     Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
45                   805                    810                    815

     gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg   2496
     Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
                     820                    825                    830
50
     gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc   2544
     Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
                     835                    840                    845

55   ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac   2592
     Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
                     850                    855                    860

     aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc   2640
60   Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
     865                    870                    875                    880

     agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg   2688
     Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
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                    885                    890                    895

   gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg   2736
   Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
 5             900                    905                    910

   gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa   2784
   Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
10             915                    920                    925

   gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac   2832
   Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
               930                    935                    940

15 ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg   2880
   Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
   945                    950                    955                    960

   gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag   2928
20 Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                       965                    970                    975

   tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg   2976
   Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
25                    980                    985                    990

   gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa   3024
   Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
30             995                    1000                   1005

   cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca   3072
   Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
       1010                   1015                   1020

35 cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg   3120
   Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
   1025                   1030                   1035                   1040

   ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga   3168
40 Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                   1045                   1050                   1055

   gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg   3216
   Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
45             1060                   1065                   1070

   cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc   3264
   His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
50         1075                   1080                   1085

   agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc   3312
   Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
       1090                   1095                   1100

55 ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat   3360
   Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
   1105                   1110                   1115                   1120

   gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac   3408
60 Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                   1125                   1130                   1135

   cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac   3456
   His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
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                    1140                    1145                    1150

      ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc   3504
      Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
  5            1155                    1160                    1165


      cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca   3552
      Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
            1170                    1175                    1180
 10

      ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg   3600
      Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
      1185                    1190                    1195                    1200

 15   gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa   3648
      Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                  1205                    1210                    1215


      gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc   3696
 20   Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
                  1220                    1225                    1230


      tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt   3744
      Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
 25            1235                    1240                    1245


      cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc   3792
      His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
            1250                    1255                    1260
 30

      atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac   3840
      Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
      1265                    1270                    1275                    1280

 35   ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc   3888
      Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                  1285                    1290                    1295


      acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc   3936
 40   Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
                  1300                    1305                    1310


      tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg   3984
      Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
 45            1315                    1320                    1325


      gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg   4032
      Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
            1330                    1335                    1340
 50

      gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg   4080
      Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
      1345                    1350                    1355                    1360

 55   ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga   4128
      Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                  1365                    1370                    1375


      ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc   4176
 60   Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
                  1380                    1385                    1390


      aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc   4224
      Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
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                1395                    1400                    1405

      ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac    4272
      Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
 5       1410                1415                1420

      acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
      Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
10    1425            1430                1435                1440

      tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
      Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

15    tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
      Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
                  1460                1465                1470

      gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
20    Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
                1475                1480                1485

      aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
      Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
25       1490                1495                1500

      ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
      Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
      1505                1510                1515                1520
30
      aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
      Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                  1525                1530                1535

35    aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag    4656
      Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
                1540                1545                1550

      atg gcc gaa gcc cag tgc aag ccc tac tac tct gac tac tcg aga ttc    4704
40    Met Ala Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
                1555                1560                1565

      cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac ctc ttc    4752
      Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
45       1570                1575                1580

      atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg gaa cat    4800
      Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
50    1585                1590                1595                1600

      tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc aat tac    4848
      Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
                1605                1610                1615

55    atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc    4896
      Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala
                1620                1625                1630

      ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg gac ctg    4944
60    Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
                1635                1640                1645

      gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag att gag    4992
      Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu
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            1650                  1655                  1660

     gtc aat ctg tcg ctg ccc atc aac ccc acc atc atc cgt atc atg agg      5040
     Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
 5   1665               1670                  1675                  1680

     gtg ctc cgc att gct cga gtt ctg aag ctg ttg aag atg gct gtg ggc      5088
     Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
10                      1685                  1690                  1695

     atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag gtg ggg      5136
     Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln Val Gly
                        1700                  1705                  1710

15   aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca gct ctg      5184
     Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
                1715                  1720                  1725

20   ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac cct tgt      5232
     Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
         1730                  1735                  1740

     gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg gcc ttt      5280
     Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
25   1745               1750                  1755                  1760

     ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt att atg      5328
     Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
                1765                  1770                  1775
30
     aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac act      5376
     Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
                     1780                  1785                  1790

35   gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt      5424
     Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
             1795                  1800                  1805

     gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg gaa gaa      5472
40   Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
         1810                  1815                  1820

     agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag ctg gag      5520
     Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu
45   1825               1830                  1835                  1840

     ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg ggc agc      5568
     Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
                     1845                  1850                  1855
50
     ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac agc cct      5616
     Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro
                1860                  1865                  1870

55   aag cct ggg gct cca cac acc act gcc cac att gga gca gcc tcg ggc      5664
     Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala Ser Gly
             1875                  1880                  1885

     ttc tcc ctt gag cac ccc acg atg gta ccc cac ccc gag gag gtg cca      5712
60   Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu Val Pro
         1890                  1895                  1900

     gtc ccc cta gga cca gac ctg ctg act gtg agg aag tct ggt gtc agc      5760
     Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser
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        1905                 1910                 1915                 1920

      cgg acg cac tct ctg ccc aat gac agc tac atg tgc cgc aat ggg agc    5808
5     Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser
                     1925                 1930                 1935

      act gct gag aga tcc cta gga cac agg ggc tgg ggg ctc ccc aaa gcc    5856
      Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala
                 1940                 1945                 1950
10
      cag tca ggc tcc atc ttg tcc gtt cac tcc caa cca gca gac acc agc    5904
      Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser
                 1955                 1960                 1965
15
      tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg ctc cag cct cat    5952
      Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln Pro His
             1970                 1975                 1980

      ggg gct ccc acc tgg ggc gcc atc cct aaa cta ccc cca cct ggc cgc    6000
20    Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg
      1985                 1990                 1995                 2000

      tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata agg act    6048
      Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr
25                   2005                 2010                 2015

      gac tcc ctg gat gtg cag ggc ctg ggt agc cgg gaa gac ctg ttg tca    6096
      Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser
                 2020                 2025                 2030
30
      gag gtg agt ggg ccc tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg    6144
      Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp
                 2035                 2040                 2045

35    ggc ggg tcg agc atc cag gtg cag cag cgt tcc ggc atc cag agc aaa    6192
      Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys
             2050                 2055                 2060

      gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc    6240
40    Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro
      2065                 2070                 2075                 2080

      agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag ctg gac    6288
      Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp
45                   2085                 2090                 2095

      acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc cag gaa    6336
      Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu
                 2100                 2105                 2110
50
      gaa ccc ctg ttc cca cgg gac ctg aag aag tgc tac agt gta gag acc    6384
      Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr
             2115                 2120                 2125

55    cag agc tgc agg cgc agg cct ggg ttc tgg cta gat gaa cag cgg aga    6432
      Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg
             2130                 2135                 2140

      cac tcc att gct gtc agc tgt ctg gac agc ggc tcc caa ccc cgc cta    6480
60    His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu
      2145                 2150                 2155                 2160

      tgt cca agc ccc tca agc ctc ggg ggc caa cct ctt ggg ggt cct ggg    6528
      Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly
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                  2165                    2170                    2175

     agc cgg cct aag aaa aaa ctc agc cca ccc agt atc tct ata gac ccc    6576
     Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro
 5            2180                2185                2190

     ccg gag agc cag ggc tct cgg ccc cca tgc agt cct ggt gtc tgc ctc    6624
     Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu
             2195                2200                2205
10

     agg agg agg gcg ccg gcc agt gac tct aag gat ccc tcg gtc tcc agc    6672
     Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser
          2210                2215                2220

15   ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac acg ctg    6720
     Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu
     2225                2230                2235                2240

     agt ctc tct ggt ttg tct tct gac cca aca gac atg gac ccc           6762
20   Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro
                    2245                2250
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25   <210> 6
     <211> 6795
     <212> DNA
     <213> Rattus sp.

     <220>
30   <221> CDS
     <222> (1)..(6795)

     <400> 6
     atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc      48
35   Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
     1               5                   10                  15

     cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag      96
     Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
40                  20                  25                  30

     ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg     144
     Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
                 35                  40                  45
45

     gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg     192
     Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
             50                  55                  60

50   agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac     240
     Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
     65                  70                  75                  80

     ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg     288
55   Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                     85                  90                  95

     act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag     336
     Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
60                  100                 105                 110

     cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt     384
     Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
                 115                 120                 125
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gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag        432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130             135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttc ttc att gtc        480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145             150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc        528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac        576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg        624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
            195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc        672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg        720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag        768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct        816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg        864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
            275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc        912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat        960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac        1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca        1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc        1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
            355                 360                 365

ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc        1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
            370                 375                 380
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ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag    1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc    1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
        405                 410                 415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc    1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc    1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
            435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg    1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
        450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc    1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac    1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc    1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg    1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg    1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
        530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac    1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca    1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act    1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg    1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
            595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc    1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
        610                 615                 620

cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt    1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640
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acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag      1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                     650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg      2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                660                     665                 670

aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca      2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
                675                     680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac      2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
                690                     695             700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat      2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                     710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca      2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                     730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc      2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
                740                     745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag      2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
                755                     760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc      2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
                770                     775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc      2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                     790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg      2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                     810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg      2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
                820                     825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc      2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
                835                     840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac      2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
                850                     855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc      2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                     870                 875                 880

agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg      2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                885                     890                 895
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     gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg    2736
     Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
             900                 905                 910
 5
     gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa    2784
     Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
             915                 920                 925
10
     gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac    2832
     Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
             930                 935                 940

     ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg    2880
15   Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
     945                 950                 955                 960

     gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag    2928
     Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
20                       965                 970                 975

     tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg    2976
     Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
                 980                 985                 990
25
     gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa    3024
     Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
                 995                 1000                1005

30   cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca    3072
     Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
         1010                1015                1020

     cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg    3120
35   Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
     1025                1030                1035                1040

     ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga    3168
     Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
40                       1045                1050                1055

     gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg    3216
     Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
                 1060                1065                1070
45
     cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc    3264
     His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
             1075                1080                1085

50   agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc    3312
     Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
             1090                1095                1100

     ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat    3360
55   Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
     1105                1110                1115                1120

     gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac    3408
     Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
60                       1125                1130                1135

     cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac    3456
     His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
                 1140                1145                1150
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ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc     3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
        1155                1160                1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca     3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
        1170                1175                1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg     3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
   1185                 1190                1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa     3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                1210                1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc     3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
             1220                1225                1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt     3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                1240                1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc     3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
        1250                1255                1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac     3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
   1265                 1270                1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc     3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                1290                1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc     3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
             1300                1305                1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg     3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                1320                1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg     4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
   1330                 1335                1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg     4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
   1345                 1350                1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga     4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
        1365                1370                1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc     4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
             1380                1385                1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc     4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
        1395                1400                1405
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      ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac    4272
      Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
          1410            1415                1420

      acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
      Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
      1425            1430                1435                1440

      tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
      Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
              1445                1450                1455

      tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
      Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
              1460                1465                1470

      gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
      Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
              1475                1480                1485

      aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
      Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
          1490                1495                1500

      ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
      Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
      1505                1510                1515                1520

      aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
      Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                  1525                1530                1535

      aag cga cta cgg agg ctg gag aaa aag aga agg aat cta atg ttg gac    4656
      Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp
              1540                1545                1550

      gat gta att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag    4704
      Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln
              1555                1560                1565

      tgc aag ccc tac tac tct gac tac tcg aga ttc cgg ctc ctt gtc cac    4752
      Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His
          1570                1575                1580

      cac ctg tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc    4800
      His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile
      1585                1590                1595                1600

      ggg ctg aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag    4848
      Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln
                  1605                1610                1615

      atc ctg gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc    4896
      Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile
              1620                1625                1630

      ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt    4944
      Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg
              1635                1640                1645

      ttc ttc cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg    4992
      Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu
              1650                1655                1660
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tcc atc atg ggc atc aca ctg gag gag att gag gtc aat ctg tcg ctg    5040
Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu
1665          1670              1675              1680

ccc atc aac ccc acc atc atc cgt atc atg agg gtg ctc cgc att gct    5088
Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala
          1685              1690              1695

cga gtt ctg aag ctg ttg aag atg gct gtg ggc atg cgg gca ctg ctg    5136
Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu
          1700              1705              1710

cac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc    5184
His Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu
          1715              1720              1725

ttc atg tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt    5232
Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe
     1730              1735              1740

gga gac ctg gag tgt gat gag aca cac cct tgt gag ggc ttg ggt cgg    5280
Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg
1745              1750              1755              1760

cat gcc acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga    5328
His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg
          1765              1770              1775

gtc tcc act ggt gac aac tgg aat ggt att atg aag gac acc ctc cgg    5376
Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg
          1780              1785              1790

gac tgt gac cag gag tcc acc tgc tac aac act gtc atc tcc cct atc    5424
Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile
          1795              1800              1805

tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg    5472
Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val
     1810              1815              1820

gtc ata gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc    5520
Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala
1825              1830              1835              1840

aag gag gag gcc gag ctc gag gcc gag ctg gag ctg gag atg aag acg    5568
Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr
          1845              1850              1855

ctc agc ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc    5616
Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro
          1860              1865              1870

ggg gtg gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca    5664
Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro
          1875              1880              1885

cac acc act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac    5712
His Thr Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His
          1890              1895              1900

ccc acg atg gta ccc cac ccc gag gag gtg cca gtc ccc cta gga cca    5760
Pro Thr Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro
1905              1910              1915              1920
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      gac ctg ctg act gtg agg aag tct ggt gtc agc cgg acg cac tct ctg   5808
      Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
                    1925                1930                1935
  5
      ccc aat gac agc tac atg tgc cgc aat ggg agc act gct gag aga tcc   5856
      Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser
                1940            1945                1950
 10
      cta gga cac agg ggc tgg ggg ctc ccc aaa gcc cag tca ggc tcc atc   5904
      Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile
            1955                1960                1965

      ttg tcc gtt cac tcc caa cca gca gac acc agc tgc atc cta cag ctt   5952
 15   Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu
            1970                1975                1980

      ccc aaa gat gtg cac tat ctg ctc cag cct cat ggg gct ccc acc tgg   6000
      Pro Lys Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp
 20   1985                1990                1995                2000

      ggc gcc atc cct aaa cta ccc cca cct ggc cgc tcc cct ctg gct cag   6048
      Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
                    2005                2010                2015
 25
      agg cct ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg   6096
      Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
                    2020                2025                2030

 30   cag ggc ctg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc   6144
      Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro
                2035                2040                2045

      tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg tcg agc atc   6192
 35   Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile
            2050                2055                2060

      cag gtg cag cag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc   6240
      Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile
 40   2065                2070                2075                2080

      cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc agc tgg gcc aag gac   6288
      Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp
                    2085                2090                2095
 45
      cct cca gag acc aga agc agc tta gag ctg gac acg gag ctg agc tgg   6336
      Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
                    2100                2105                2110

 50   att tca gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttc cca   6384
      Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro
                    2115                2120                2125

      cgg gac ctg aag aag tgc tac agt gta gag acc cag agc tgc agg cgc   6432
 55   Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg
            2130                2135                2140

      agg cct ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gct gtc   6480
      Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val
 60   2145                2150                2155                2160

      agc tgt ctg gac agc ggc tcc caa ccc cgc cta tgt cca agc ccc tca   6528
      Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser
                    2165                2170                2175
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agc ctc ggg ggc caa cct ctt ggg ggt cct ggg agc cgg cct aag aaa    6576
Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys
            2180                2185                2190

aaa ctc agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc    6624
Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly
        2195                2200                2205

tct cgg ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg    6672
Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro
    2210                2215                2220

gcc agt gac tct aag gat ccc tcg gtc tcc agc ccc ctt gac agc acg    6720
Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr
2225                2230                2235                2240

gct gcc tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg    6768
Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu
            2245                2250                2255

tct tct gac cca aca gac atg gac ccc                                6795
Ser Ser Asp Pro Thr Asp Met Asp Pro
            2260                2265
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1               5                   10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag    96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg    144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg    192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac    240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg    288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag    336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
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cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt    384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag    432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
        130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc    480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc    528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                    165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
                180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg    624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
                195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc    672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
        210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg    720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag    768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                    245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct    816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg    864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
                275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc    912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
        290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat    960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac   1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                    325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca   1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc   1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
                355                 360                 365
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ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc    1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370             375             380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag    1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385             390             395             400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc    1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405             410             415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc    1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                420             425             430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc    1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
            435             440             445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg    1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
        450             455             460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc    1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465             470             475             480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac    1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485             490             495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc    1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500             505             510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg    1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515             520             525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg    1632
Ser Arg Arg Leu Met Leu Pro Pro Ser Thr Pro Thr Pro Ser Gly
        530             535             540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac    1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545             550             555             560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca    1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565             570             575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act    1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                580             585             590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg    1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
            595             600             605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc    1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
        610             615             620
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cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt    1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag    1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                    645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg    2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                660                 665                 670

aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca    2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
            675                 680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac    2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
            690                 695                 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat    2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca    2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc    2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
                740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag    2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
            755                 760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc    2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc    2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg    2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg    2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
                820                 825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc    2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
            835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac    2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc    2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880
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    agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg   2688
    Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                    885                 890                 895

5   gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg   2736
    Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
                    900                 905                 910

10  gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa   2784
    Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
                    915                 920                 925

    gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac   2832
    Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
15          930                 935                 940

    ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg   2880
    Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
    945                 950                 955                 960
20
    gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag   2928
    Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                    965                 970                 975

25  tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg   2976
    Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
                    980                 985                 990

30  gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa   3024
    Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
                    995                 1000                1005

    cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca   3072
    Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
35          1010                1015                1020

    cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg   3120
    Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
    1025                1030                1035                1040
40
    ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga   3168
    Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                    1045                1050                1055

45  gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg   3216
    Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
                    1060                1065                1070

    cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc   3264
50  His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
                    1075                1080                1085

    agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc   3312
    Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
55          1090                1095                1100

    ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat   3360
    Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
    1105                1110                1115                1120
60
    gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac   3408
    Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                    1125                1130                1135
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cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac   3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
            1140              1145              1150

ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc   3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
            1155              1160              1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca   3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
            1170              1175              1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg   3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
            1185              1190              1195              1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa   3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
            1205              1210              1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc   3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220              1225              1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt   3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
            1235              1240              1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc   3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
            1250              1255              1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac   3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
            1265              1270              1275              1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc   3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
            1285              1290              1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc   3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300              1305              1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg   3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
            1315              1320              1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg   4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
            1330              1335              1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg   4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
            1345              1350              1355              1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga   4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
            1365              1370              1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc   4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380              1385              1390
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aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc   4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
    1395                1400                1405

ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac   4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
    1410                1415                1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga   4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
    1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg   4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat   4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
                1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac   4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
    1475                1480                1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc   4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
    1490                1495                1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat   4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
    1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag   4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag   4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
                1540                1545                1550

atg gcc gat cta atg ttg gac gat gta att gct tcc ggc agc tca gcc   4704
Met Ala Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala
    1555                1560                1565

agc gct gcg tca gaa gcc cag tgc aag ccc tac tac tct gac tac tcg   4752
Ser Ala Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser
    1570                1575                1580

aga ttc cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac   4800
Arg Phe Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp
    1585                1590                1595                1600

ctc ttc atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg   4848
Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met
                1605                1610                1615

gaa cat tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc   4896
Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys
                1620                1625                1630

aat tac atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt   4944
Asn Tyr Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu
                1635                1640                1645
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      gtg gcc ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg     4992
      Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu
      1650                1655                1660

 5    gac ctg gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag     5040
      Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu
      1665                1670                1675                1680

10    att gag gtc aat ctg tcg ctg ccc atc aac ccc acc atc atc cgt atc     5088
      Ile Glu Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile
                       1685                1690                1695

      atg agg gtg ctc cgc att gct cga gtt ctg aag ctg ttg aag atg gct     5136
15    Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala
                  1700                1705                1710

      gtg ggc atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag     5184
      Val Gly Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln
20                1715                1720                1725

      gtg ggg aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca     5232
      Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala
             1730                1735                1740

25    gct ctg ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac     5280
      Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His
      1745                1750                1755                1760

30    cct tgt gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg     5328
      Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met
                       1765                1770                1775

      gcc ttt ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt     5376
35    Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly
                  1780                1785                1790

      att atg aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac     5424
      Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr
                  1795                1800                1805
40
      aac act gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc     5472
      Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala
      1810                1815                1820

45    cag ttt gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg     5520
      Gln Phe Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu
      1825                1830                1835                1840

      gaa gaa agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag     5568
50    Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu
                       1845                1850                1855

      ctg gag ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg     5616
      Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu
55                1860                1865                1870

      ggc agc ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac     5664
      Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp
             1875                1880                1885
60
      agc cct aag cct ggg gct cca cac acc act gcc cac att gga gca gcc     5712
      Ser Pro Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala
             1890                1895                1900
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63

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tcg ggc ttc tcc ctt gag cac ccc acg atg gta ccc cac cct gag gag    5760
Ser Gly Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu
1905            1910            1915            1920

gtg cca gtc ccc cta gga cca gac ctg ctg act gtg agg aag tct ggt    5808
Val Pro Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly
            1925            1930            1935

gtc agc cgg acg cac tct ctg ccc aat gac agc tac atg tgc cgc aat    5856
Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn
        1940            1945            1950

ggg agc act gct gag aga tcc cta gga cac agg ggc tgg ggg ctc ccc    5904
Gly Ser Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro
        1955            1960            1965

aaa gcc cag tca ggc tcc atc ttg tcc gtt cac tcc caa cca gca gac    5952
Lys Ala Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp
        1970            1975            1980

acc agc tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg ctc cag    6000
Thr Ser Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln
1985            1990            1995            2000

cct cat ggg gct ccc acc tgg ggc gcc atc cct aaa cta ccc cca cct    6048
Pro His Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro
            2005            2010            2015

ggc cgc tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata    6096
Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile
        2020            2025            2030

agg act gac tcc ctg gat gtg cag ggc ctg ggt agc cgg gaa gac ctg    6144
Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu
        2035            2040            2045

ttg tca gag gtg agt ggg ccc tcc tgc cct ctg acc cgg tcc tca tcc    6192
Leu Ser Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser
        2050            2055            2060

ttc tgg ggc ggg tcg agc atc cag gtg cag cag cgt tcc ggc atc cag    6240
Phe Trp Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln
2065            2070            2075            2080

agc aaa gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg    6288
Ser Lys Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu
            2085            2090            2095

gaa ccc agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag    6336
Glu Pro Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu
            2100            2105            2110

ctg gac acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc    6384
Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser
        2115            2120            2125

cag gaa gaa ccc ctg ttc cca cgg gac ctg aag aag tgc tac agt gta    6432
Gln Glu Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val
        2130            2135            2140

gag acc cag agc tgc agg cgc agg cct ggg ttc tgg cta gat gaa cag    6480
Glu Thr Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln
2145            2150            2155            2160
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cgg aga cac tcc att gct gtc agc tgt ctg gac agc ggc tcc caa ccc    6528
Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro
            2165                    2170                    2175

cgc cta tgt cca agc ccc tca agc ctc ggg ggc caa cct ctt ggg ggt    6576
Arg Leu Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly
            2180                    2185                    2190

cct ggg agc cgg cct aag aaa aaa ctc agc cca ccc agt atc tct ata    6624
Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile
            2195                    2200                    2205

gac ccc ccg gag agc cag ggc tct cgg ccc cca tgc agt cct ggt gtc    6672
Asp Pro Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val
            2210                    2215                    2220

tgc ctc agg agg agg gcg ccg gcc agt gac tct aag gat ccc tcg gtc    6720
Cys Leu Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val
2225                    2230                    2235                    2240

tcc agc ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac    6768
Ser Ser Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp
            2245                    2250                    2255

acg ctg agt ctc tct ggt ttg tct tct gac cca aca gac atg gac ccc    6816
Thr Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro
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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
  1               5                   10                  15

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Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
            20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg    144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
            35                  40                  45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg    192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
            50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg tc tgt aac    240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg    288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag    336
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        Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
                    100                 105                 110

        cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt    384
        Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
                115                 120                 125

        gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc att ttt ggg aag    432
        Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
            130                 135                 140

        aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc    480
        Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
        145                 150                 155                 160

        att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc    528
        Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                        165                 170                 175

        tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
        Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
                    180                 185                 190

        cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg    624
        Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
                195                 200                 205

        cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc    672
        Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
            210                 215                 220

        ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg    720
        Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
        225                 230                 235                 240

        tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag    768
        Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                        245                 250                 255

        cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct    816
        Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
                    260                 265                 270

        cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg    864
        Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
                275                 280                 285

        cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc    912
        Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
            290                 295                 300

        tat aac agt tcc agc aac acc acc tgt gtt aac tgg aac cag tac tat    960
        Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
        305                 310                 315                 320

        acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac   1008
        Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                        325                 330                 335

        ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca   1056
        Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
                    340                 345                 350

        ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc   1104
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          Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
              355                     360                 365

    5     ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc    1152
          Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
              370                 375                 380

          ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag    1200
   10     Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
          385                 390                 395                 400

          acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc    1248
          Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
   15                         405                 410                 415

          ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc    1296
          Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
                          420                 425                 430

   20     tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc    1344
          Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
                      435                 440                 445

          cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg    1392
   25     Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
                  450                 455                 460

          ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc    1440
          Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
   30     465                 470                 475                 480

          agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac    1488
          Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
   35                     485                 490                 495

          cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc    1536
          His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
                          500                 505                 510

   40     aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg    1584
          Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
                      515                 520                 525

          tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg    1632
   45     Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
                  530                 535                 540

          ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac    1680
   50     Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
          545                 550                 555                 560

          tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca    1728
          Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
   55                     565                 570                 575

          tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act    1776
          Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
                      580                 585                 590

   60     gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg    1824
          Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
                      595                 600                 605

          gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc    1872
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    Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
        610             615             620

 5  cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt  1920
    Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
    625             630             635             640

10  acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag  1968
    Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645             650             655

    gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg  2016
    Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
                660             665             670
15
    aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca  2064
    Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
                675             680             685

20  gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac  2112
    Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
                690             695             700

25  ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat  2160
    Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
    705             710             715             720

    gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca  2208
    Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725             730             735
30
    ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc  2256
    Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
                740             745             750
35
    gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag  2304
    Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
                755             760             765

40  ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc  2352
    Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
        770             775             780

45  agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc  2400
    Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
    785             790             795             800

    ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg  2448
    Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805             810             815
50
    gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg  2496
    Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
                820             825             830
55
    gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc  2544
    Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
                835             840             845

60  ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac  2592
    Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
        850             855             860

    aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc  2640
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         Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
         865             870             875             880

     5   agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg   2688
         Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                         885             890             895

         gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg   2736
    10   Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
                         900             905             910

         gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa   2784
         Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
                         915             920             925
    15
         gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac   2832
         Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
                         930             935             940

    20   ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg   2880
         Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
         945             950             955             960

         gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag   2928
    25   Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                         965             970             975

         tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg   2976
         Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
    30                   980             985             990

         gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa   3024
         Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
                         995             1000            1005
    35
         cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca   3072
         Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
                 1010            1015            1020

    40   cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg   3120
         Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
         1025            1030            1035            1040

         ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga   3168
    45   Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                 1045            1050            1055

         gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg   3216
         Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
    50           1060            1065            1070

         cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc   3264
         His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
                 1075            1080            1085
    55
         agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc   3312
         Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
                 1090            1095            1100

    60   ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat   3360
         Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
                 1105            1110            1115            1120

         gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac   3408
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       Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
                1125                    1130                  1135

  5    cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac    3456
       His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
                1140                    1145                  1150

       ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc    3504
 10    Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
                1155                    1160                  1165

       cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca    3552
       Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
                1170                    1175                  1180
 15
       ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg    3600
       Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
       1185                1190                1195                1200

 20    gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa    3648
       Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                    1210                  1215

       gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc    3696
 25    Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
                1220                    1225                  1230

       tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt    3744
       Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
 30             1235                    1240                  1245

       cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc    3792
       His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
 35             1250                    1255                  1260

       atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac    3840
       Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
       1265                1270                1275                1280

 40    ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc    3888
       Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                    1290                  1295

       acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc    3936
 45    Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
                1300                    1305                  1310

       tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg    3984
       Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
 50             1315                    1320                  1325

       gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg    4032
       Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
 55             1330                    1335                  1340

       gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg    4080
       Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
       1345                1350                1355                1360

 60    ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga    4128
       Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                1365                    1370                  1375

       ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc    4176
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        Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
              1380                    1385                 1390

  5     aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc    4224
        Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
              1395                    1400                 1405

        ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag gct gag gac    4272
 10     Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
              1410                    1415                 1420

        acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
        Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
        1425                1430                1435                1440
 15
        tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
        Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                     1445                 1450                 1455

 20     tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
        Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
                   1460                 1465                 1470

        gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
 25     Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
                  1475                 1480                 1485

        aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
        Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
 30           1490                 1495                 1500

        ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
        Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
 35     1505                1510                1515                1520

        aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
        Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                     1525                 1530                 1535

 40     aag cga cta cgg agg ctg gag aaa aag aga agg aaa gcc cag tgc aag    4656
        Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys
                   1540                 1545                 1550

        ccc tac tac tct gac tac tcg aga ttc cgg ctc ctt gtc cac cac ctg    4704
 45     Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
                  1555                 1560                 1565

        tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc ggg ctg    4752
        Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
 50           1570                 1575                 1580

        aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag atc ctg    4800
        Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
 55     1585                1590                1595                1600

        gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc ttt gtc    4848
        Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
                     1605                 1610                 1615

 60     ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt ttc ttc    4896
        Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
                   1620                 1625                 1630

        cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg tcc atc    4944
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        Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
             1635                1640                 1645

  5     atg ggc atc aca ctg gag gag att gag gtc aat ctg tcg ctg ccc atc    4992
        Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu Pro Ile
             1650                1655                1660

 10     aac ccc acc atc atc cgt atc atg agg gtg ctc cgc att gct cga gtt    5040
        Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val
        1665                1670                1675                1680

        ctg aag ctg ttg aag atg gct gtg ggc atg cgg gca ctg ctg cac acg    5088
        Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu His Thr
                        1685                 1690                1695
 15
        gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg    5136
        Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met
                   1700                1705                1710

 20     tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac    5184
        Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp
             1715                1720                1725

 25     ctg gag tgt gat gag aca cac cct tgt gag ggc ttg ggt cgg cat gcc    5232
        Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
             1730                1735                1740

        acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga gtc tcc    5280
        Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser
 30     1745                1750                1755                1760

        act ggt gac aac tgg aat ggt att atg aag gac acc ctc cgg gac tgt    5328
        Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys
                        1765                1770                1775
 35
        gac cag gag tcc acc tgc tac aac act gtc atc tcc cct atc tac ttt    5376
        Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
                   1780                1785                1790

 40     gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg gtc ata    5424
        Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
             1795                1800                1805

 45     gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc aag gag    5472
        Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
        1810                1815                1820

        gag gcc gag ctc gag gcc gag ctg gag ctg gag atg aag acg ctc agc    5520
        Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
 50     1825                1830                1835                1840

        ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc ggg gtg    5568
        Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
                   1845                1850                1855
 55
        gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca cac acc    5616
        Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro His Thr
             1860                1865                1870

 60     act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac ccc acg    5664
        Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His Pro Thr
             1875                1880                1885

        atg gta ccc cac ccc gag gag gtg cca gtc ccc cta gga cca gac ctg    5712
```

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      Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro Asp Leu
         1890                1895                1900

 5    ctg act gtg agg aag tct ggt gtc agc cgg acg cac tct ctg ccc aat    5760
      Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn
      1905                1910                1915                1920

      gac agc tac atg tgc cgc aat ggg agc act gct gag aga tcc cta gga    5808
10    Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser Leu Gly
                       1925                1930                1935

      cac agg ggc tgg ggg ctc ccc aaa gcc cag tca ggc tcc atc ttg tcc    5856
      His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile Leu Ser
15                   1940                1945                1950

      gtt cac tcc caa cca gca gac acc agc tgc atc cta cag ctt ccc aaa    5904
      Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu Pro Lys
                  1955                1960                1965

20    gat gtg cac tat ctg ctc cag cct cat ggg gct ccc acc tgg ggc gcc    5952
      Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp Gly Ala
         1970                1975                1980

      atc cct aaa cta ccc cca cct ggc cgc tcc cct ctg gct cag agg cct    6000
25    Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro
      1985                1990                1995                2000

      ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg cag ggc    6048
      Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly
30                   2005                2010                2015

      ctg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc tcc tgc    6096
      Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro Ser Cys
35                   2020                2025                2030

      cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg tcg agc atc cag gtg    6144
      Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile Gln Val
                  2035                2040                2045

40    cag cag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc cgc ctg    6192
      Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile Arg Leu
         2050                2055                2060

      cca gcc cct tgc cca ggc ctg gaa ccc agc tgg gcc aag gac cct cca    6240
45    Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp Pro Pro
      2065                2070                2075                2080

      gag acc aga agc agc tta gag ctg gac acg gag ctg agc tgg att tca    6288
      Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser
50                   2085                2090                2095

      gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttc cca cgg gac    6336
      Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro Arg Asp
55                   2100                2105                2110

      ctg aag aag tgc tac agt gta gag acc cag agc tgc agg cgc agg cct    6384
      Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg Arg Pro
               2115                2120                2125

60    ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gct gtc agc tgt    6432
      Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys
         2130                2135                2140

      ctg gac agc ggc tcc caa ccc cgc cta tgt cca agc ccc tca agc ctc    6480
```

```
   Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser Ser Leu
   2145                2150                2155                2160

5  ggg ggc caa cct ctt ggg ggt cct ggg agc cgg cct aag aaa aaa ctc   6528
   Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu
                       2165                2170                2175

   agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc tct cgg   6576
   Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly Ser Arg
10                     2180                2185                2190

   ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg gcc agt   6624
   Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro Ala Ser
15             2195                2200                2205

   gac tct aag gat ccc tcg gtc tcc agc ccc ctt gac agc acg gct gcc   6672
   Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr Ala Ala
         2210                2215                2220

20 tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg tct tct   6720
   Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu Ser Ser
   2225                2230                2235                2240

   gac cca aca gac atg gac ccc                                        6741
25 Asp Pro Thr Asp Met Asp Pro
                       2245


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40 Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly
   1               5                   10                  15

   cgc cgc ccc tgg ccc tgc ggc gtt ggt ggg ggc gtc ccc gga gag ccc   96
   Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
45                 20                  25                  30

   cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca   144
   Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
50             35                  40                  45

   ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac   192
   Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
         50                  55                  60

55 gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc   240
   Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
   65                  70                  75                  80

   tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc   288
60 Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
                   85                  90                  95

   tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac   336
   Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn
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                100   105   110

      tgc gtg acc ctg ggc atg ttc cgg ccc tgt gag gac gtt gag tgc ggc   384
  5   Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys Gly
              115   120   125

      tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc   432
 10   Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
              130   135   140

      ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc   480
      Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
 15   145   150   155   160

      ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc   528
      Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
 20   165   170   175

      atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg   576
 20   Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
                  180   185   190

      agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc   624
 25   Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
              195   200   205

      atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat   672
      Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
 30   210   215   220

      acg ctg ccc atg ctc ggg aac gtc ctt ctg ctg tgc ttc ttc gtc ttc   720
      Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
      225   230   235   240

 35   ttc att ttc ggc atc gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg   768
      Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                  245   250   255

 40   aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc   816
 40   Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
              260   265   270

      ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc   864
 45   Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
              275   280   285

      atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc   912
      Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
 50   290   295   300

      ccc ggc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc   960
      Pro Gly Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
      305   310   315   320

 55   tac acg cag ccg cag gcc gag ggg gtg ggc gct gca cgc aac gcc tgc   1008
      Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
                  325   330   335

 60   atc aac tgg aac cag tac tac aac gtg tgc cgc tcg ggt gac tcc aac   1056
 60   Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
                  340   345   350

      ccc cac aac ggt gcc atc aac ttc gac aac acc tgc tac gcc tgg att   1104
      Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
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                355                    360                    365

        gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac atc atg tac      1152
        Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr
 5          370                375                380

        tac gtc atg gac gcc cac tca ttc tac aac ttc atc tat ttc atc ctg      1200
        Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
        385                390                395                400
10

        ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg      1248
        Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
                       405                410                415
15
        att gcc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg      1296
        Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
                       420                425                430

        cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc      1344
        Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
20                 435                440                445

        ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc      1392
        Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
25             450                455                460

        cac ata ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc      1440
        His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
        465                470                475                480
30
        tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc      1488
        Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                       485                490                495

        cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg      1536
35      Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
                       500                505                510

        gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac      1584
40      Val His His Leu Val Tyr His His His His His His His His Tyr
                       515                520                525

        cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc      1632
        His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
45          530                535                540

        tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc      1680
        Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
        545                550                555                560
50
        cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat      1728
        Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                       565                570                575

        gcc gac tgc cac ata gag ggg ccg cag gag agg gcc cgg gtg ggc aca      1776
55      Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
                       580                585                590

        tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg      1824
60      Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
                       595                600                605

        cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa      1872
        His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
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                610                      615                      620

      agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc   1920
      Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala
 5    625                 630                 635                 640

      agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac   1968
      Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
                          645                 650                 655
10
      gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct   2016
      Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro
                      660                 665                 670

15    ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca   2064
      Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
                  675                 680                 695

      gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt   2112
20    Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
              690                 695                 700

      gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac   2160
      Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
25    705                 710                 715                 720

      tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt   2208
      Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                          725                 730                 735
30
      gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc   2256
      Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
                      740                 745                 750

35    cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg   2304
      Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
                  755                 760                 765

      ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag   2352
40    Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
              770                 775                 780

      ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg   2400
      Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
45    785                 790                 795                 800

      gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag   2448
      Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                      805                 810                 815
50
      ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc   2496
      Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
                      820                 825                 830

55    agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct   2544
      Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
                  835                 840                 845

      ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg   2592
60    Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
              850                 855                 860

      gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct   2640
      Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser
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        865                    870                     875                     88C

        gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttc    2688
        Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
  5                         885                     890                     895

        ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac    2736
        Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp
  10                    900                     905                     910

        aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc    2784
        Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
  15                    915                     920                     925

        agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca    2832
        Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr
                        930                     935                     940

        gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg    2880
        Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
  20    945                     950                     955                     960

        tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac    2928
        Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn
  25                    965                     970                     975

        gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc    2976
        Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu
  30                    980                     985                     990

        tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg    3024
        Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
                        995                     1000                    1005

        ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac    3072
  35    Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
            1010                    1015                    1020

        aga tcc gac acg gac gag gac aag acg tcg gtc cac ttc gag gag gac    3120
  40    Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
        1025                    1030                    1035                    1040

        ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc    3168
        Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
  45                        1045                    1050                    1055

        ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc    3216
        Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
  50                    1060                    1065                    1070

        ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga    3264
        Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
                        1075                    1080                    1085

        gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg    3312
  55    Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
            1090                    1095                    1100

        gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg    3360
  60    Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
        1105                    1110                    1115                    1120

        cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg    3408
        Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp
```

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                      1125                1130                1135

      agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa    3456
      Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
 5                    1140                1145                1150

      gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag    3504
      Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
                   1155                1160                1165
10

      ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc    3552
      Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
                   1170                1175                1180

15    ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg    3600
      Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
      1185                1190                1195                1200

      ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg    3648
20    Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
                   1205                1210                1215

      cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac    3696
      Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
25                   1220                1225                1230

      cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc    3744
      Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
                   1235                1240                1245
30
      ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg    3792
      Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
                   1250                1255                1260

35    agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac    3840
      Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
      1265                1270                1275                1280

      cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat    3888
40    Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
                   1285                1290                1295

      cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg    3936
      His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
45                   1300                1305                1310

      gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc    3984
      Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
                   1315                1320                1325
50
      gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg    4032
      Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
                   1330                1335                1340

55    aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag    4080
      Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln
      1345                1350                1355                1360

      agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg    4128
60    Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
                   1365                1370                1375

      gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt    4176
      Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
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                 1380                    1385                    1390

     gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc    4224
     Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val
 5            1395                    1400                    1405

     atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca    4272
     Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
              1410                    1415                    1420
10
     tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc    4320
     Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
     1425                    1430                    1435                    1440

15   atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac    4368
     Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
                      1445                    1450                    1455

     tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc    4416
20   Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
                   1460                    1465                    1470

     cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac    4464
     Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
25            1475                    1480                    1485

     ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga    4512
     Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
              1490                    1495                    1500
30
     tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag    4560
     Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
     1505                    1510                    1515                    1520

35   cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc    4608
     Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
                   1525                    1530                    1535

     ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc    4656
40   Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
                   1540                    1545                    1550

     gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag    4704
     Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
45            1555                    1560                    1565

     gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc    4752
     Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
              1570                    1575                    1580
50
     agg agc act ttc ccc agc cca gag gcc cag cgc cgg ccc tac tat gcc    4800
     Arg Ser Thr Phe Pro Ser Pro Glu Ala Gln Arg Arg Pro Tyr Tyr Ala
     1585                    1590                    1595                    1600

55   gac tac tcg ccc acg cgc cgc tgg att cac tcg ctg tgc acc agc cac    4848
     Asp Tyr Ser Pro Thr Arg Arg Trp Ile His Ser Leu Cys Thr Ser His
                      1605                    1610                    1615

     tat ctc gac ctc ttc atc acc ttc atc atc tgt gtc aac gtc atc acc    4896
60   Tyr Leu Asp Leu Phe Ile Thr Phe Ile Ile Cys Val Asn Val Ile Thr
                   1620                    1625                    1630

     atg tcc atg gag cac tat aac caa ccc aag tcg ctg gac gag gcc ctc    4944
     Met Ser Met Glu His Tyr Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu
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            1635                  1640                  1645

     aag tac tgc aac tac gtc ttc acc atc gtg ttt gtc ttc gag gct gca    4992
     Lys Tyr Cys Asn Tyr Val Phe Thr Ile Val Phe Val Phe Glu Ala Ala
 5       1650                  1655                  1660

     ctg aag ctg gta gca ttt ggg ttc cgt cgg ttc ttc aag gac agg tgg    5040
     Leu Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp
10   1665                  1670               1675                  1680

     aac cag ctg gac ctg gcc atc gtg ctg ctg tca ctc atg ggc atc acg    5088
     Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Leu Met Gly Ile Thr
                     1685                  1690                  1695

15   ctg gag gag ata gag atg agc gcc gcg ctg ccc atc aac ccc acc atc    5136
     Leu Glu Glu Ile Glu Met Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile
                 1700                  1705                  1710

     atc cgc atc atg cgc gtg ctt cgc att gcc cgt gtg ctg aag ctg ctg    5184
20   Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu
             1715                  1720                  1725

     aag atg gct acg ggc atg cgc gcc ctg ctg gac act gtg gtg caa gct    5232
     Lys Met Ala Thr Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala
25       1730                  1735                  1740

     ctc ccc cag gtg ggg aac ctg ggc ctt ctt ttc atg ctc ctg ttt ttt    5280
     Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe
     1745                  1750                  1755                  1760
30
     atc tat gct gcg ctg gga gtg gag ctg ttc ggg agg ctg gag tgc agt    5328
     Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe Gly Arg Leu Glu Cys Ser
                 1765                  1770                  1775

35   gaa gac aac ccc tgc gag ggc ctg agc agg cac gcc acc ttc agc aac    5376
     Glu Asp Asn Pro Cys Glu Gly Leu Ser Arg His Ala Thr Phe Ser Asn
                 1780                  1785                  1790

     ttc ggc atg gcc ttc ctc acg ctg ttc cgc gtg tcc acg ggg gac aac    5424
40   Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn
             1795                  1800                  1805

     tgg aac ggg atc atg aag gac acg ctg cgc gag tgc tcc cgt gag gac    5472
     Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp
45       1810                  1815                  1820

     aag cac tgc ctg agc tac ctg ccg gcc ccg tcg ccc gtc tac ttc gtg    5520
     Lys His Cys Leu Ser Tyr Leu Pro Ala Pro Ser Pro Val Tyr Phe Val
     1825                  1830                  1835                  1840
50
     acc ttc gtg ctg gtg ccc cag ttc gtg ctg gtg aac gtg gtg gtg gcc    5568
     Thr Phe Val Leu Val Pro Gln Phe Val Leu Val Asn Val Val Val Ala
                     1845                  1850                  1855

55   gtg ctc atg aag cac ctg gag gag agc aac aag gag gct cgg gag gat    5616
     Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp
                 1860                  1865                  1870

     gcg gag ctg gac gcc gag atc gag ctg gag atg gcg cag ggc ccc ggg    5664
60   Ala Glu Leu Asp Ala Glu Ile Glu Leu Glu Met Ala Gln Gly Pro Gly
                 1875                  1880                  1885

     agt gca cgc cgg gtg gac gcg gac agg cct ccc ttg ccc cag gag agt    5712
     Ser Ala Arg Arg Val Asp Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser
```

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            1890                    1895                    1900

      ccg ggc gcc agg gac gcc cca aac ctg gtt gca cgc aag gtg tcc gtg    5760
      Pro Gly Ala Arg Asp Ala Pro Asn Leu Val Ala Arg Lys Val Ser Val
 5    1905                    1910                    1915                    1920


      tcc agg atg ctc tcg ctg ccc aac gac agc tac atg ttc agg ccc gtg    5808
      Ser Arg Met Leu Ser Leu Pro Asn Asp Ser Tyr Met Phe Arg Pro Val
                          1925                    1930                    1935
10

      gtg cct gcc tcg gcg ccc cac ccc cgc ccg ctg cag gag gtg gag atg    5856
      Val Pro Ala Ser Ala Pro His Pro Arg Pro Leu Gln Glu Val Glu Met
                    1940                    1945                    1950

15    gag acc tat ggg gcc ggc acc ccc ttg ggc tcc gtt gcc tct gtg cac    5904
      Glu Thr Tyr Gly Ala Gly Thr Pro Leu Gly Ser Val Ala Ser Val His
                    1955                    1960                    1965


      tct ccg ccc gca gag tcc tgt gcc tcc ctc cag atc cca ctg gct gtg    5952
20    Ser Pro Pro Ala Glu Ser Cys Ala Ser Leu Gln Ile Pro Leu Ala Val
                    1970                    1975                    1980


      tcg tcc cca gcc agg agc ggc gag ccc ctc cac gcc ctg tcc cct cgg    6000
      Ser Ser Pro Ala Arg Ser Gly Glu Pro Leu His Ala Leu Ser Pro Arg    --
25    1985                    1990                    1995                    2000


      ggc aca gcc cgc tcc ccc agt ctc agc cgg ctg ctc tgc aga cag gag    6048
      Gly Thr Ala Arg Ser Pro Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu
                    2005                    2010                    2015
30

      gct gtg cac acc gat tcc ttg aag gga aga ttg aca gcc cta ggg aca    6096
      Ala Val His Thr Asp Ser Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr
                    2020                    2025                    2030

35    ccc tgg atc ctg cag agc ctg gtg aga aaa ccc cgg                    6132
      Pro Trp Ile Leu Gln Ser Leu Val Arg Lys Pro Arg                    --
                    2035                    2040



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      Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly
      1               5                   10                  15


      cgc cgc ccc tgg ccc tgc ggc gtt ggt ggg ggc gtc ccc gga gag ccc    96
55    Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
                      20                  25                  30


      cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca    144
      Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
60                35                  40                  45


      ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac    192
      Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
                    50                  55                  60
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       gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc   240
       Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
 5      65                  70                  75                  80

       tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc   288
       Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
                        85                  90                  95

10     tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac   336
       Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn
                    100                 105                 110

       tgc gtg acc ctg ggc atg ttc cgg ccc tgt gag gac gtt gag tgc ggc   384
15     Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys Gly
                    115                 120                 125

       tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc   432
       Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
20         130                 135                 140

       ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc   480
       Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
25     145                 150                 155                 160

       ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc   528
       Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
                        165                 170                 175

30     atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg   576
       Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
                    180                 185                 190

       agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc   624
35     Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
                    195                 200                 205

       atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat   672
       Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
40         210                 215                 220

       acg ctg ccc atg ctc ggg aac gtc ctt ctg ctg tgc ttc ttc gtc ttc   720
       Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
       225                 230                 235                 240
45

       ttc att ttc ggc atc gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg   768
       Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                        245                 250                 255

50     aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc   816
       Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
                    260                 265                 270

       ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc   864
55     Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
                    275                 280                 285

       atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc   912
       Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
60         290                 295                 300

       ccc ggc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc   960
       Pro Gly Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
       305                 310                 315                 320
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    tac acg cag ccg cag gcc gag ggg gtg ggt gct gca cgc aac gcc tgc    1008
    Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
5                   325             330             335

    atc aac tgg aac cag tac tac aac gtg tgc cgc tcg ggt gac tcc aac    1056
    Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
                    340             345             350

10  ccc cac aac ggt gcc atc aac ttc gac aac acc tgc tac gcc tgg att    1104
    Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
                    355             360             365

    gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac atc atg tac    1152
15  Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr
                    370             375             380

    tac gtc atg gac gcc cac tca ttc tac aac ttc atc tat ttc atc ctg    1200
    Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
20  385             390             395             400

    ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg    1248
    Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
                    405             410             415
25

    att gcc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg    1296
    Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
                    420             425             430

30  cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc    1344
    Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
                    435             440             445

    ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc    1392
35  Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
                    450             455             460

    cac ata ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc    1440
    His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
40  465             470             475             480

    tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc    1488
    Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                    485             490             495
45

    cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg    1536
    Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
                    500             505             510

50  gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac    1584
    Val His His Leu Val Tyr His His His His His His His His His Tyr
                    515             520             525

    cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc    1632
55  His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
                    530             535             540

    tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc    1680
    Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
60  545             550             555             560

    cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat    1728
    Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                    565             570             575
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   gcc gac tgc cac ata gag ggg ccg cag gag agg gcc cgg gtg ggc aca   1776
   Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
               580                 585                 590

   tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg   1824
   Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
               595                 600                 605

   cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa   1872
   His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
               610                 615                 620

   agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc   1920
   Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala
   625                 630                 635                 640

   agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac   1968
   Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
                       645                 650                 655

   gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct   2016
   Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro
               660                 665                 670

   ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca   2064
   Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
               675                 680                 685

   gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt   2112
   Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
               690                 695                 700

   gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac   2160
   Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
   705                 710                 715                 720

   tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt   2208
   Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                       725                 730                 735

   gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc   2256
   Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
               740                 745                 750

   cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg   2304
   Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
               755                 760                 765

   ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag   2352
   Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
               770                 775                 780

   ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg   2400
   Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
   785                 790                 795                 800

   gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag   2448
   Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                       805                 810                 815

   ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc   2496
   Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
               820                 825                 830
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      agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct    2544
      Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
              835             840                 845

      ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg    2592
      Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
          850                 855                 860

      gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct    2640
      Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser
      865             870                 875                 880

      gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttt    2688
      Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
                  885                 890                 895

      ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac    2736
      Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp
                  900                 905                 910

      aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc    2784
      Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
              915                 920                 925

      agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca    2832
      Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr
          930                 935                 940

      gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg    2880
      Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
      945             950                 955                 960

      tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac    2928
      Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn
                  965                 970                 975

      gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc    2976
      Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu
                  980                 985                 990

      tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg    3024
      Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
              995                 1000                1005

      ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac    3072
      Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
          1010                1015                1020

      aga tcc gac acg gac gag gac aag acg tcg gtc cac ttc gag gag gac    3120
      Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
      1025                1030                1035                1040

      ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc    3168
      Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
                  1045                1050                1055

      ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc    3216
      Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
                  1060                1065                1070

      ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga    3264
      Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
                  1075                1080                1085
```

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     gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg    3312
     Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
5        1090               1095                1100

     gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg    3360
     Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
     1105                1110                1115                1120

10   cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg    3408
     Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp
                     1125                1130                1135

     agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa    3456
15   Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
                     1140                1145                1150

     gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag    3504
     Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
20       1155                1160                1165

     ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc    3552
     Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
25       1170                1175                1180

     ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg    3600
     Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
     1185                1190                1195                1200

30   ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg    3648
     Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
                     1205                1210                1215

     cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac    3696
35   Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
                     1220                1225                1230

     cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc    3744
     Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
40       1235                1240                1245

     ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg    3792
     Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
45       1250                1255                1260

     agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac    3840
     Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
     1265                1270                1275                1280

50   cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat    3888
     Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
                     1285                1290                1295

     cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg    3936
55   His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
                     1300                1305                1310

     gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc    3984
     Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
60       1315                1320                1325

     gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg    4032
     Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
         1330                1335                1340
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aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag    4080
Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln
1345                1350                1355                1360

agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg    4128
Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
             1365                1370                1375

gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt    4176
Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
          1380                1385                1390

gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc    4224
Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val
          1395                1400                1405

atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca    4272
Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
     1410                1415                1420

tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc    4320
Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
1425                1430                1435                1440

atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac    4368
Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
             1445                1450                1455

tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc    4416
Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
          1460                1465                1470

cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac    4464
Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
          1475                1480                1485

ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga    4512
Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
     1490                1495                1500

tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag    4560
Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
1505                1510                1515                1520

cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc    4608
Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
             1525                1530                1535

ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc    4656
Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
             1540                1545                1550

gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag    4704
Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
          1555                1560                1565

gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc    4752
Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
     1570                1575                1580

agg aag gcc cag cgc cgg ccc tac tat gcc gac tac tcg ccc acg cgc    4800
Arg Lys Ala Gln Arg Arg Pro Tyr Tyr Ala Asp Tyr Ser Pro Thr Arg
1585                1590                1595                1600
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cgc tgg att cac tcg ctg tgc acc agc cac tat ctc gac ctc ttc atc      4848
Arg Trp Ile His Ser Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile
                1605                1610                1615

acc ttc atc atc tgt gtc aac gtc atc acc atg tcc atg gag cac tat      4896
Thr Phe Ile Ile Cys Val Asn Val Ile Thr Met Ser Met Glu His Tyr
                1620                1625                1630

aac caa ccc aag tcg ctg gac gag gcc ctc aag tac tgc aac tac gtc      4944
Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu Lys Tyr Cys Asn Tyr Val
                1635                1640                1645

ttc acc atc gtg ttt gtc ttc gag gct gca ctg aag ctg gta gca ttt      4992
Phe Thr Ile Val Phe Val Phe Glu Ala Ala Leu Lys Leu Val Ala Phe
                1650                1655                1660

ggg ttc cgt cgg ttc ttc aag gac agg tgg aac cag ctg gac ctg gcc      5040
Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp Asn Gln Leu Asp Leu Ala
                1665                1670                1675                1680

atc gtg ctg ctg tca ctc atg ggc atc acg ctg gag gag ata gag atg      5088
Ile Val Leu Leu Ser Leu Met Gly Ile Thr Leu Glu Glu Ile Glu Met
                1685                1690                1695

agc gcc gcg ctg ccc atc aac ccc acc atc atc cgc atc atg cgc gtg      5136
Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val
                1700                1705                1710

ctt cgc att gcc cgt gtg ctg aag ctg ctg aag atg gct acg ggc atg      5184
Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr Gly Met
                1715                1720                1725

cgc gcc ctg ctg gac act gtg gtg caa gct ctc ccc cag gtg ggg aac      5232
Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val Gly Asn
                1730                1735                1740

ctg ggc ctt ctt ttc atg ctc ctg ttt ttt atc tat gct gcg ctg gga      5280
Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly
                1745                1750                1755                1760

gtg gag ctg ttc ggg agg ctg gag tgc agt gaa gac aac ccc tgc gag      5328
Val Glu Leu Phe Gly Arg Leu Glu Cys Ser Glu Asp Asn Pro Cys Glu
                1765                1770                1775

ggc ctg agc agg cac gcc acc ttc agc aac ttc ggc atg gcc ttc ctc      5376
Gly Leu Ser Arg His Ala Thr Phe Ser Asn Phe Gly Met Ala Phe Leu
                1780                1785                1790

acg ctg ttc cgc gtg tcc acg ggg gac aac tgg aac ggg atc atg aag      5424
Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys
                1795                1800                1805

gac acg ctg cgc gag tgc tcc cgt gag gac aag cac tgc ctg agc tac      5472
Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp Lys His Cys Leu Ser Tyr
                1810                1815                1820

ctg ccg gcc ccg tcg ccc gtc tac ttc gtg acc ttc gtg ctg gtg ccc      5520
Leu Pro Ala Pro Ser Pro Val Tyr Phe Val Thr Phe Val Leu Val Pro
                1825                1830                1835                1840

cag ttc gtg ctg gtg aac gtg gtg gtg gcc gtg ctc atg aag cac ctg      5568
Gln Phe Val Leu Val Asn Val Val Val Ala Val Leu Met Lys His Leu
                1845                1850                1855
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        gag gag agt aac aag gag gct cgg gag gat gcg gag ctg gac gcc gag    5616
        Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp Ala Glu Leu Asp Ala Glu
  5             1860                1865                1870

        atc gag ctg gag atg gcg cag ggc ccc ggg agt gca cgc cgg gtg gac    5664
        Ile Glu Leu Glu Met Ala Gln Gly Pro Gly Ser Ala Arg Arg Val Asp
                1875                1880                1885

 10     gcg gac agg cct ccc ttg ccc cag gag agt ccg ggc gcc agg gac gcc    5712
        Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser Pro Gly Ala Arg Asp Ala
                1890                1895                1900

        cca aac ctg gtt gca cgc aag gtg tcc gtg tcc agg atg ctc tcg ctg    5760
 15     Pro Asn Leu Val Ala Arg Lys Val Ser Val Ser Arg Met Leu Ser Leu
        1905                1910                1915                1920

        ccc aac gac agc tac atg ttc agg ccc gtg gtg cct gcc tcg gcg ccc    5808
        Pro Asn Asp Ser Tyr Met Phe Arg Pro Val Val Pro Ala Ser Ala Pro
 20                 1925                1930                1935

        cac ccc cgc ccg ctg cag gag gtg gag atg gag acc tat ggg gcc ggc    5856
        His Pro Arg Pro Leu Gln Glu Val Glu Met Glu Thr Tyr Gly Ala Gly
 25             1940                1945                1950

        acc ccc ttg ggc tcc gtt gcc tct gtg cac tct ccg ccc gca gag tcc    5904
        Thr Pro Leu Gly Ser Val Ala Ser Val His Ser Pro Pro Ala Glu Ser
                1955                1960                1965

 30     tgt gcc tcc ctc cag atc cca ctg gct gtg tcg tcc cca gcc agg agc    5952
        Cys Ala Ser Leu Gln Ile Pro Leu Ala Val Ser Ser Pro Ala Arg Ser
        1970                1975                1980

        ggc gag ccc ctc cac gcc ctg tcc cct cgg ggc aca gcc cgc tcc ccc    6000
 35     Gly Glu Pro Leu His Ala Leu Ser Pro Arg Gly Thr Ala Arg Ser Pro
        1985                1990                1995                2000

        agt ctc agc cgg ctg ctc tgc aga cag gag gct gtg cac acc gat tcc    6048
        Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu Ala Val His Thr Asp Ser
 40             2005                2010                2015

        ttg aag gga aga ttg aca gcc cta ggg aca ccc tgg atc ctg cag agc    6096
        Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr Pro Trp Ile Leu Gln Ser
                2020                2025                2030
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        ctg gtg aga aaa ccc cgg                                            6114
        Leu Val Arg Lys Pro Arg
                2035

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        Met Ala Glu Ser Ala Ser Pro Pro Ser Ser Ser Ala Ala Ala Pro Ala
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gct gag cca gga gtc acc acg gag cag ccc gga ccc cgg agc ccc cca    96
Ala Glu Pro Gly Val Thr Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro
            20                  25                  30

tcc tcc ccg cca ggc ctg gag gag cct ctg gat gga gct gat cct cat   144
Ser Ser Pro Pro Gly Leu Glu Glu Pro Leu Asp Gly Ala Asp Pro His
        35                  40                  45

gtc cca cac cca gac ctg gcg cct att gcc ttc ttc tgc ctg cga cag   192
Val Pro His Pro Asp Leu Ala Pro Ile Ala Phe Phe Cys Leu Arg Gln
        50                  55                  60

acc acc agc ccc cgg aac tgg tgc atc aag atg gtg tgc aac ccg tgg   240
Thr Thr Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp
65                  70                  75                  80

ttt gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt   288
Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu
                    85                  90                  95

ggc atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc   336
Gly Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys
            100                 105                 110

aag atc atg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg   384
Lys Ile Met Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met
            115                 120                 125

gag atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc   432
Glu Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys
        130                 135                 140

tac ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca   480
Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala
145                 150                 155                 160

ggg atg gtc gag tac tcc ctg gac ctt cag aac atc aac ctg tca gcc   528
Gly Met Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala
                    165                 170                 175

atc cgc acc gtg cgc gtc ctg agg ccc ctc aaa gcc atc aac cgc gtg   576
Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val
            180                 185                 190

ccc agt atg cgg atc ctg gtg aac ctg ctc ctg gac aca ctg ccc atg   624
Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met
            195                 200                 205

ctg ggg aat gtc ctg ctg ctc tgc ttc ttt gtc ttc ttc atc ttt ggc   672
Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly
        210                 215                 220

atc ata ggt gtg cag ctc tgg gcg ggc ctg ctg cgt aac cgc tgc ttc   720
Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe
225                 230                 235                 240

ctg gag gag aac ttc acc ata caa ggg gat gtg gcc ttg ccc cca tac   768
Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr
                    245                 250                 255

tac cag ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg tcg   816
Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser
            260                 265                 270
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ggc gac aat ggg ata atg ggc tgc cat gag atc ccc ccg ctc aag gag    864
Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu
        275                 280                 285

cag ggc cgt gag tgc tgc ctg tcc aag gac gac gtc tac gac ttt ggg    912
Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly
        290                 295                 300

gcg ggg cgc cag gac ctc aat gcc agc ggc ctc tgt gtc aac tgg aac    960
Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn
305                 310                 315                 320

cgt tac tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt   1008
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly
                325                 330                 335

gcc atc aac ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag   1056
Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln
            340                 345                 350

gtg atc act ctg gaa ggc tgg gtg gag atc atg tac tac gtg atg gat   1104
Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
        355                 360                 365

gct cac tcc ttc tac aac ttc atc tac ttc atc ctg ctt atc ata gtg   1152
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val
        370                 375                 380

ggc tcc ttc ttc atg atc aac ctg tgc ctc gtt gtc ata gcg acc cag   1200
Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln
385                 390                 395                 400

ttc tcg gag acc aag caa cgg gag cac cgg ctg atg ctg gag cag cgg   1248
Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg
                405                 410                 415

cag cgc tac ctg tcc tcc agc acg gtg gcc agc tac gcc gag cct ggc   1296
Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly
            420                 425                 430

gac tgc tac gag gag atc ttc cag tat gtc tgc cac atc ctg cgc aag   1344
Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys
        435                 440                 445

gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg cag agc cgg cgc   1392
Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg
        450                 455                 460

cag gcc ctg ggc ccg gag gcc ccg gcc ccc gcc aaa cct ggg ccc cac   1440
Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His
465                 470                 475                 480

gcc aag gag ccc cgg cac tac cag ctg tgc ccg caa cat agc ccc ctg   1488
Ala Lys Glu Pro Arg His Tyr Gln Leu Cys Pro Gln His Ser Pro Leu
                485                 490                 495

gat gcg acg ccc cac acc ctg gtg cag ccc atc ccc gcc acg ctg gcc   1536
Asp Ala Thr Pro His Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala
            500                 505                 510

tcc gat ccc gcc agc tgc cct tgc tgc cag cat gag gac ggc cgg cgg   1584
Ser Asp Pro Ala Ser Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg
        515                 520                 525
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ccc tcg ggc ctg ggc agc acc gac tcg ggc cag gag ggc tcg ggc tcc    1632
Pro Ser Gly Leu Gly Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser
    530                 535                 540

ggg agc tcc gct ggt ggc gag gac gag gcg gat ggg gac ggg gcc cgg    1680
Gly Ser Ser Ala Gly Gly Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg
545                 550                 555                 560

agc agc gag gac gga gcc tcc tca gaa ctg ggg aag gag gag gag gag    1728
Ser Ser Glu Asp Gly Ala Ser Ser Glu Leu Gly Lys Glu Glu Glu Glu
                565                 570                 575

gag gag cag gcg gat ggg gcg gtc tgg ctg tgc ggg gat gtg tgg cgg    1776
Glu Glu Gln Ala Asp Gly Ala Val Trp Leu Cys Gly Asp Val Trp Arg
                580                 585                 590

gag acg cga gcc aag ctg cgc ggc atc gtg gac agc aag tac ttc aac    1824
Glu Thr Arg Ala Lys Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn
            595                 600                 605

cgg ggc atc atg atg gcc atc ctg gtc aac acc gtc agc atg ggc atc    1872
Arg Gly Ile Met Met Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile
        610                 615                 620

gag cac cac gag cag ccg gag gag ctg acc aac atc ctg gag atc tgc    1920
Glu His His Glu Gln Pro Glu Glu Leu Thr Asn Ile Leu Glu Ile Cys
625                 630                 635                 640

aat gtg gtc ttc acc agc atg ttt gcc ctg gag atg atc ctg aag ctg    1968
Asn Val Val Phe Thr Ser Met Phe Ala Leu Glu Met Ile Leu Lys Leu
                645                 650                 655

gct gca ttt ggg ctc ttc gac tac ctg cgt aac ccc tac aac atc ttc    2016
Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn Ile Phe
                660                 665                 670

gac agc atc att gtc atc atc agc atc tgg gag atc gtg ggg cag gcg    2064
Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly Gln Ala
            675                 680                 685

gac ggt ggg ctg tcg gtg ctg cgg acc ttc cgg ctg ctg cgc gtg ctg    2112
Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu
        690                 695                 700

aaa ctg gtg cgc ttc atg cct gcc ctg cgg cgc cag ctc gtg gtg ctc    2160
Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val Val Leu
705                 710                 715                 720

atg aag acc atg gac aac gtg gcc acc ttc tgc atg ctg ctc atg ctc    2208
Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu
                725                 730                 735

ttc atc ttc atc ttc agc atc ctt ggg atg cat att ttt ggc tgc aag    2256
Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly Cys Lys
                740                 745                 750

ttc agc ctc cgc acg gac act gga gac acg gtg ccc gac agg aag aac    2304
Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn
                755                 760                 765

ttc gac tcc ctg ctg tgg gcc atc gtc act gtg ttc cag atc ctc acc    2352
Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr
                770                 775                 780
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cag gag gac tgg aac gtc gtt ctc tac aat ggc atg gcc tcc act tct     2400
Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser
785             790             795             800

ccc tgg gcc tcc ctc tac ttt gtc gcc ctc atg acc ttc ggc aac tat     2448
Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr
            805             810             815

gtg ctc ttc aac ctg ctg gtg gcc atc ctg gtg gag ggc ttc cag gcg     2496
Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala
        820             825             830

gag ggt gac gcc aat cgc tcc tac tcg gac gag gac cag agc tca tcc     2544
Glu Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser Ser Ser
        835             840             845

aac ata gaa gag ttt gat aag ctc cag gaa ggc ctg gac agc agc gga     2592
Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser Gly
    850             855             860

gat ccc aag ctc tgc cca atc ccc atg acc ccc aat ggg cac ctg gac     2640
Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His Leu Asp
865             870             875             880

ccc agt ctc cca ctg ggt ggg cac cta ggt cct gct ggg gct gcg gga     2688
Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala Gly
            885             890             895

cct gcc ccc cga ctc tca ctg cag ccg gac ccc atg ctg gtg gcc ctg     2736
Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala Leu
        900             905             910

ggc tcc cga aag agc agc gtc atg tct cta ggg agg atg agc tat gac     2784
Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser Tyr Asp
        915             920             925

cag cgc tcc ctg tcc agc tcc cgg agc tcc tac tac ggg cca tgg ggc     2832
Gln Arg Ser Leu Ser Ser Ser Arg Ser Ser Tyr Tyr Gly Pro Trp Gly
930             935             940

cgc agc gcg gcc tgg gcc agc cgt cgc tcc agc tgg aac agc ctc aag     2880
Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser Ser Trp Asn Ser Leu Lys
945             950             955             960

cac aag ccg ccg tcg gcg gag cat gag tcc ctg ctc tct gcg gag cgc     2928
His Lys Pro Pro Ser Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg
            965             970             975

ggc ggc ggc gcc cgg gtc tgc gag gtt gcc gcg gac gag ggg ccg ccg     2976
Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro
            980             985             990

cgg gcc gca ccc ctg cac acc cca cac gcc cac cac gtt cat cac ggg     3024
Arg Ala Ala Pro Leu His Thr Pro His Ala His His Val His His Gly
        995             1000            1005

ccc cat ctg gcg cac cgc cac cgc cac cac cgc cgg acg ctg tcc ctc     3072
Pro His Leu Ala His Arg His Arg His His Arg Arg Thr Leu Ser Leu
    1010            1015            1020

gac aac agg gac tcg gtg gac ctg gcc gag ctg gtg ccc gcg gtg ggc     3120
Asp Asn Arg Asp Ser Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly
1025            1030            1035            1040
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```
gcc cac ccc cgg gcc gcc tgg agg gcg gca ggc ccg gcc ccc ggg cat    3168
Ala His Pro Arg Ala Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His
            1045                    1050                    1055

gag gac tgc aat ggc agg atg ccc agc atc gcc aaa gac gtc ttc acc    3216
Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr
            1060                    1065                    1070

aag atg ggc gac cgc ggg gat cgc ggg gag gat gag gag gaa atc gac    3264
Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp
            1075                    1080                    1085

tac acc ctg tgc ttc cgc gtc cgc aag atg atc gac gtc tat aag ccc    3312
Tyr Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro
        1090                    1095                    1100

gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc    3360
Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro
1105                    1110                    1115                    1120

gag aac agg ttc cgg gtc ctg tgt cag acc atc att gcc cac aaa ctc    3408
Glu Asn Arg Phe Arg Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu
            1125                    1130                    1135

ttc gac tac gtc gtc ctg gcc ttc atc ttt ctc aac tgc atc acc atc    3456
Phe Asp Tyr Val Val Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile
            1140                    1145                    1150

gcc ctg gag cgg cct cag atc gag gcc ggc agc acc gaa cgc atc ttt    3504
Ala Leu Glu Arg Pro Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe
            1155                    1160                    1165

ctc acc gtg tcc aac tac atc ttc acg gcc atc ttc gtg ggc gag atg    3552
Leu Thr Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met
        1170                    1175                    1180

aca ttg aag gta gtc tcg ctg ggc ctg tac ttc ggc gag cag gcg tac    3600
Thr Leu Lys Val Val Ser Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr
1185                    1190                    1195                    1200

cta cgc agc agc tgg aac gtg ctg gat ggc ttt ctt gtc ttc gtg tcc    3648
Leu Arg Ser Ser Trp Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser
            1205                    1210                    1215

atc atc gac atc gtg gtg tcc ctg gcc tca gcc ggg gga gcc aag atc    3696
Ile Ile Asp Ile Val Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile
            1220                    1225                    1230

ttg ggg gtc ctc cga gtc ttg cgg ctc ctg cgc acc cta cgc ccc ctg    3744
Leu Gly Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu
            1235                    1240                    1245

cgt gtc atc agc cgg gcg ccg ggc ctg aag ctg gtg gtg gag aca ctc    3792
Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu
        1250                    1255                    1260

atc tcc tcc ctc aag ccc atc ggc aac atc gtg ctc atc tgc tgt gcc    3840
Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala
1265                    1270                    1275                    1280

ttc ttc atc atc ttt ggc atc ctg gga gtg cag ctc ttc aag ggc aag    3888
Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys
            1285                    1290                    1295
```

```
ttc tac cac tgt ctg ggc gtg gac acc cgc aac atc acc aac cgc tcg    3936
Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile Thr Asn Arg Ser
            1300                1305                1310

gac tgc atg gcc gcc aac tac cgc tgg gtc cat cac aaa tac aac ttc    3984
Asp Cys Met Ala Ala Asn Tyr Arg Trp Val His His Lys Tyr Asn Phe
            1315                1320                1325

gac aac ctg ggc cag gct ctg atg tcc ctc ttt gtc ctg gca tcc aag    4032
Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ala Ser Lys
            1330                1335                1340

gat ggt tgg gtg aac atc atg tac aat gga ctg gat gct gtt gct gtg    4080
Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp Ala Val Ala Val
      1345                1350                1355                1360

gac cag cag cct gtg acc aac cac aac ccc tgg atg ctg ctg tac ttc    4128
Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met Leu Leu Tyr Phe
                  1365                1370                1375

atc tcc ttc ctg ctc atc gtc agc ttc ttt gtg ctc aac atg ttt gtg    4176
Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val
            1380                1385                1390

ggt gtc gtg gtg gag aac ttc cac aag tgc cgg cag cac cag gag gct    4224
Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln His Gln Glu Ala
            1395                1400                1405

gaa gag gca cgg cgg cgt gag gag aag cgg ctg cgg cgc ctg gag aag    4272
Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys
            1410                1415                1420

aag cgc cgg aag gcc cag cgg ctg ccc tac tat gcc acc tat tgt cac    4320
Lys Arg Arg Lys Ala Gln Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys His
      1425                1430                1435                1440

acc cgg ctg ctc atc cac tcc atg tgc acc agc cac tac ctg gac atc    4368
Thr Arg Leu Leu Ile His Ser Met Cys Thr Ser His Tyr Leu Asp Ile
                  1445                1450                1455

ttc atc acc ttc atc atc tgc ctc aac gtg gtc acc atg tcc ctg gag    4416
Phe Ile Thr Phe Ile Ile Cys Leu Asn Val Val Thr Met Ser Leu Glu
            1460                1465                1470

cac tac aat cag ccc acg tcc ctg gag aca gcc ctc aag tac tgc aac    4464
His Tyr Asn Gln Pro Thr Ser Leu Glu Thr Ala Leu Lys Tyr Cys Asn
            1475                1480                1485

tat atg ttc acc act gtc ttt gtg ctg gag gct gtg ctg aag ctg gtg    4512
Tyr Met Phe Thr Thr Val Phe Val Leu Glu Ala Val Leu Lys Leu Val
            1490                1495                1500

gca ttt ggt ctg agg cgc tta ttc aag gac cga tgg aac cag ctg gac    4560
Ala Phe Gly Leu Arg Arg Leu Phe Lys Asp Arg Trp Asn Gln Leu Asp
      1505                1510                1515                1520

ctg gcc att gtg cta ctg tca gtc atg ggc atc acc ctg gag gag atc    4608
Leu Ala Ile Val Leu Leu Ser Val Met Gly Ile Thr Leu Glu Glu Ile
                  1525                1530                1535

gag atc aat gcg gcc ctg ccc atc aat ccc acc atc atc cgc atc atg    4656
Glu Ile Asn Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met
            1540                1545                1550
```

```
agg gtt ctg cgc att gcc cga gtg ctg aag ctg ttg aag atg gcc aca    4704
Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr
        1555                1560                1565
```

```
gga atg cgg gcc ctg ctg gac acg gtg gtg caa gct ttg ccc cag gtg    4752
Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val
        1570                1575                1580
```

```
ggc aac ctg ggc ctc ctc ttc atg ctg ctc ttc ttc atc tat gct gct    4800
Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala
    1585                1590                1595                1600
```

```
ctc ggg gtg gag ctc ttt ggg aag ctg gtc tgc aac gac gag aac ccg    4848
Leu Gly Val Glu Leu Phe Gly Lys Leu Val Cys Asn Asp Glu Asn Pro
                1605                1610                1615
```

```
tgc gag ggc atg agc cgg cat gcc acc ttc gag aac ttc ggc atg gcc    4896
Cys Glu Gly Met Ser Arg His Ala Thr Phe Glu Asn Phe Gly Met Ala
            1620                1625                1630
```

```
ttc ctc aca ctc ttc cag gtc tcc acg ggt gac aac tgg aac ggg atc    4944
Phe Leu Thr Leu Phe Gln Val Ser Thr Gly Asp Asn Trp Asn Gly Ile
        1635                1640                1645
```

```
atg aag gac acg ctg cgg gac tgc acc cac gac gag cgc agc tgc ctg    4992
Met Lys Asp Thr Leu Arg Asp Cys Thr His Asp Glu Arg Ser Cys Leu
        1650                1655                1660
```

```
agc agc ctg cag ttt gtg tcg ccg ctg tac ttc gtg agc ttc gtg ctc    5040
Ser Ser Leu Gln Phe Val Ser Pro Leu Tyr Phe Val Ser Phe Val Leu
    1665                1670                1675                1680
```

```
acc gcg cag ttc gtg ctc atc aac gtg gtg gtg gct gtg ctc atg aag    5088
Thr Ala Gln Phe Val Leu Ile Asn Val Val Val Ala Val Leu Met Lys
                1685                1690                1695
```

```
cac ctg gac gac agc aac aag gag gcg cag gag gac gcc gag atg gat    5136
His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp Ala Glu Met Asp
            1700                1705                1710
```

```
gcc gag ctc gag ctg gag atg gcc cat ggc ctg ggc cct ggc ccg agg    5184
Ala Glu Leu Glu Leu Glu Met Ala His Gly Leu Gly Pro Gly Pro Arg
        1715                1720                1725
```

```
ctg cct acc ggc tcc ccg ggc gcc cct ggc cga ggg ccg gga ggg gcg    5232
Leu Pro Thr Gly Ser Pro Gly Ala Pro Gly Arg Gly Pro Gly Gly Ala
        1730                1735                1740
```

```
ggc ggc ggg ggc gac acc gat ggc ggc ttg tgc cgg cgc tgc tac tcg    5280
Gly Gly Gly Gly Asp Thr Asp Gly Gly Leu Cys Arg Arg Cys Tyr Ser
    1745                1750                1755                1760
```

```
cct gcc cag gag aac ctg tgg ctg gac agc gtc tct tta atc atc aag    5328
Pro Ala Gln Glu Asn Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys
                1765                1770                1775
```

```
gac tcc ttg gag ggg gag ctg acc atc atc gac aac ctg tcg ggc tcc    5376
Asp Ser Leu Glu Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser
            1780                1785                1790
```

```
atc ttc cac cac tac tcc tcg cct gcc ggc tgc aag aag tgt cac cac    5424
Ile Phe His His Tyr Ser Ser Pro Ala Gly Cys Lys Lys Cys His His
        1795                1800                1805
```

```
gac aag caa gag aca ggt cct cgt cca tcc tgc tgg gtg acg acc        5469
Asp Lys Gln Glu Thr Gly Pro Arg Pro Ser Cys Trp Val Thr Thr
    1810                1815                1820
```

<210> 12
<211> 5505
<212> DNA
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<220>
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<222> (1)..(5505)

<400> 12

```
atg gct gac agc aac tta ccg ccc tca tct gca gca gcc ccg gcc cct        48
Met Ala Asp Ser Asn Leu Pro Pro Ser Ser Ala Ala Ala Pro Ala Pro
  1               5                  10                  15
```

```
gag ccg gga atc act gag cag ccg ggg ccc cgg agt ccc cct cca tcc        96
Glu Pro Gly Ile Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro Pro Ser
               20                  25                  30
```

```
cct cca ggc ctg gag gag cca ttg gaa gga acc aac cct gac gtc cca       144
Pro Pro Gly Leu Glu Glu Pro Leu Glu Gly Thr Asn Pro Asp Val Pro
            35                  40                  45
```

```
cat cca gac ctg gct cct gtt gct ttc ttc tgc ctg cgc cag acc acg       192
His Pro Asp Leu Ala Pro Val Ala Phe Phe Cys Leu Arg Gln Thr Thr
        50                  55                  60
```

```
agc cca cgg aac tgg tgc atc aag atg gtt tgt aac ccg tgg ttc gag       240
Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp Phe Glu
    65                  70                  75                  80
```

```
tgt gtg agc atg ctg gtt att ctg ctg aac tgt gtg acc ctg ggc atg       288
Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met
                85                  90                  95
```

```
tac cag cca tgt gat gac atg gag tgc ctg tcg gac cgt tgc aag atc       336
Tyr Gln Pro Cys Asp Asp Met Glu Cys Leu Ser Asp Arg Cys Lys Ile
              100                 105                 110
```

```
ctg cag gtc ttc gat gac ttc atc ttc atc ttc ttt gcc atg gag atg       384
Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met
          115                 120                 125
```

```
gtg ctt aag atg gtg gcc ctg ggc att ttt ggc aag aag tgc tac ctc       432
Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu
      130                 135                 140
```

```
gga gac aca tgg aac cgc ctg gat ttc ttc att gtc atg gca ggg atg       480
Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Met
145                 150                 155                 160
```

```
gtt gag tac tct ctg gac cta cag aac atc aac ctg tca gcc atc cgc       528
Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala Ile Arg
                165                 170                 175
```

```
act gtg cgt gtc ctg agg cct ctc aaa gcc atc aac cgt gta ccc agc       576
Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val Pro Ser
              180                 185                 190
```

```
atg cgg atc ctg gtg aac ctg ctg ctc gac acg ctg ccc atg ctg ggg       624
```

```
                    Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly
                            195                     200                 205

  5    aac gtg ctc ctg ctc tgt ttc ttc gtc ttc ttc atc ttc ggc atc att        672
       Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile
                210                     215                 220

  10   ggc gtg cag ctc tgg gca ggc ctg cta cgg aac cgc tgc ttc ctg gaa        720
       Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
       225                     230                 235                 240

       gag aac ttc acc ata caa ggg gat gtg gcc ctg ccc cct tat tac caa        768
       Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
                            245                 250                 255
  15
       cca gag gag gat gac gag atg ccc ttt atc tgc tcc ctg act ggg gac        816
       Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
                            260                 265                 270

  20   aat ggc atc atg ggc tgc cac gag atc ccc cca ctg aag gag cag ggc        864
       Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
                    275                     280                 285

  25   cgg gaa tgc tgc ctg tcc aaa gat gat gtg tat gac ttc ggg gcg ggg        912
       Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
                290                     295                 300

  30   cgc cag gac ctc aac gcc agc ggt ctg tgc gtc aac tgg aac cgc tac        960
       Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
       305                     310                 315                 320

       tac aac gtc tgc cgc acg ggc aac gcc aac cct cac aag ggc gcc atc       1008
       Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile
                            325                 330                 335
  35
       aac ttt gac aac att ggc tat gcc ggg att gtg att ttc cag gtg atc       1056
       Asn Phe Asp Asn Ile Gly Tyr Ala Gly Ile Val Ile Phe Gln Val Ile
                            340                 345                 350

  40   act ctg gaa ggc tgg gtg gag atc atg tac tat gtg atg gac gca cat       1104
       Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His
                    355                     360                 365

  45   tct ttc tac aac ttc atc tac ttc att ctg ctc atc ata gtg ggc tcc       1152
       Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser
                370                     375                 380

       ttc ttc atg atc aac ttg tgc ctc gtt gtc ata gca acc cag ttc tct       1200
       Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser
  50   385                     390                 395                 400

       gag acc aag caa cgg gag cac cgg ctg atg ctg gag caa cgc cag cgc       1248
       Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg Gln Arg
                            405                 410                 415
  55
       tac ctg tcc tcc agc acg gtg gcc agt tac gct gag ccc ggt gat tgc       1296
       Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly Asp Cys
                            420                 425                 430

  60   tat gag gag atc ttc caa tat gtc tgt cac atc ctt cgc aaa gcc aag       1344
       Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys Ala Lys
                    435                     440                 445

       cgc cgt gcc cta ggc ctc tac cag gcc ctg cag aac cgg cgc cag gcc       1392
```

```
          Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Asn Arg Arg Gln Ala
              450                 455                 460

  5       atg ggc ccg ggg aca cca gcc cct gcc aag cct ggg ccc cat gcc aag        1440
          Met Gly Pro Gly Thr Pro Ala Pro Ala Lys Pro Gly Pro His Ala Lys
          465                 470                 475                 480

          gag ccc agc cac tgc aag ctg tgc cca cga cac agc ccc ctg gac ccc        1488
 10       Glu Pro Ser His Cys Lys Leu Cys Pro Arg His Ser Pro Leu Asp Pro
                              485                 490                 495

          act ccc cac aca ctg gtg cag ccc atc tct gcc att ctg gcc tct gac        1536
          Thr Pro His Thr Leu Val Gln Pro Ile Ser Ala Ile Leu Ala Ser Asp
 15                           500                 505                 510

          ccc agc agc tgc cct cac tgc cag cac gag gca ggc agg cgg ccc tct        1584
          Pro Ser Ser Cys Pro His Cys Gln His Glu Ala Gly Arg Arg Pro Ser
                              515                 520                 525

 20       ggc ctg ggc agc act gac tca ggc cag gaa ggc tca ggt tct ggt ggc        1632
          Gly Leu Gly Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Gly
                  530                 535                 540

          tct gca gag gcc gaa gcc aat ggg gat gga ctc cag agc agt gag gat        1680
 25       Ser Ala Glu Ala Glu Ala Asn Gly Asp Gly Leu Gln Ser Ser Glu Asp
          545                 550                 555                 560

          ggg gtc tcc tcg gac ctg ggg aag gag gag gaa cag gag gac ggg gca        1728
 30       Gly Val Ser Ser Asp Leu Gly Lys Glu Glu Glu Gln Glu Asp Gly Ala
                              565                 570                 575

          gcc cga ctg tgt ggg gat gtg tgg cgc gag aca cga aaa aag ctg cgg        1776
          Ala Arg Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Lys Lys Leu Arg
 35                           580                 585                 590

          ggc atc gtg gac agc aag tac ttc aac aga ggt atc atg atg gct atc        1824
          Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met Ala Ile
                          595                 600                 605

 40       ctg gtg aac aca gtc agc atg ggc atc gag cac cac gaa cag ccc gag        1872
          Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln Pro Glu
                  610                 615                 620

          gag ctg acc aac atc ctg gag atc tgc aat gtg gtc ttc acc agt atg        1920
 45       Glu Leu Thr Asn Ile Leu Glu Ile Cys Asn Val Val Phe Thr Ser Met
          625                 630                 635                 640

          ttt gcc ctg gag atg atc ctg aaa ctg gcc gcc ttt ggg ctc ttc gac        1968
 50       Phe Ala Leu Glu Met Ile Leu Lys Leu Ala Ala Phe Gly Leu Phe Asp
                              645                 650                 655

          tac ctg cgg aac cct tac aac atc ttt gac agc atc atc gtc atc atc        2016
          Tyr Leu Arg Asn Pro Tyr Asn Ile Phe Asp Ser Ile Ile Val Ile Ile
 55                           660                 665                 670

          agc atc tgg gaa atc gtg ggg cag gcg gac ggt ggc ctg tct gtg ctg        2064
          Ser Ile Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser Val Leu
                          675                 680                 685

 60       cgc acc ttc cgg ttg ctg cgg gtg ctg aag ctg gtg cgc ttc atg ccg        2112
          Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe Met Pro
                  690                 695                 700

          gcg ctg cgg cgc cag ctc gtg gtg ctc atg aag acc atg gac aac gtg        2160
```

```
       Ala Leu Arg Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn Val
       705                 710                 715                 720

 5     gcc acc ttc tgc atg cta ctc atg ctg ttc atc ttc atc ttc agc atc   2208
       Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser Ile
                           725                 730                 735

       ctt ggg atg cat atc ttt ggc tgc aaa ttc agc ctc cgc acg gac acg   2256
10     Leu Gly Met His Ile Phe Gly Cys Lys Phe Ser Leu Arg Thr Asp Thr
                           740                 745                 750

       gga gac acc gtt cct gac agg aag aac ttc gat tcc tta ctg tgg gcc   2304
       Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
15                         755                 760                 765

       atc gtc aca gtg ttc cag atc ctc act cag gag gac tgg aac gtt gtc   2352
       Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Val Val
                           770                 775                 780

20     ctg tac aat ggc atg gcc tcc acc acc ccc tgg gcc tcc ctc tat ttt   2400
       Leu Tyr Asn Gly Met Ala Ser Thr Thr Pro Trp Ala Ser Leu Tyr Phe
       785                 790                 795                 800

       gtt gcc ctc atg acc ttt ggc aac tac gtt ctc ttc aat ctc ctg gtg   2448
25     Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
                           805                 810                 815

       gct atc ctg gta gag ggt ttc cag gct gag ggt gat gct aat cgt tcc   2496
       Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Arg Ser
30                         820                 825                 830

       tgc tct gat gag gac cag agc tca tcc aat ttg gag gag ttt gac aag   2544
       Cys Ser Asp Glu Asp Gln Ser Ser Ser Asn Leu Glu Glu Phe Asp Lys
35                         835                 840                 845

       ctc cca gag ggc ctg gac aac agt aga gat ctc aag ctc tgc cca ata   2592
       Leu Pro Glu Gly Leu Asp Asn Ser Arg Asp Leu Lys Leu Cys Pro Ile
                           850                 855                 860

40     ccc atg aca ccc aat gga cac ctg gac cct agc ctc cct ctg ggt gcg   2640
       Pro Met Thr Pro Asn Gly His Leu Asp Pro Ser Leu Pro Leu Gly Ala
       865                 870                 875                 880

       cat ctg ggt cct gct ggt acc atg ggt act gcc ccc cgc ctc tca ctg   2688
45     His Leu Gly Pro Ala Gly Thr Met Gly Thr Ala Pro Arg Leu Ser Leu
                           885                 890                 895

       cag cca gac ccg gta ctg gtg gcc cta gac tct cgg aaa agc agt gtc   2736
       Gln Pro Asp Pro Val Leu Val Ala Leu Asp Ser Arg Lys Ser Ser Val
50                         900                 905                 910

       atg tcc ctg ggc agg atg agc tat gat cag cga tcc ttg tcc agc tcc   2784
       Met Ser Leu Gly Arg Met Ser Tyr Asp Gln Arg Ser Leu Ser Ser Ser
55                         915                 920                 925

       cgg agc tcc tac tac ggg ccc tgg ggc cgc agt ggg acc tgg gct agc   2832
       Arg Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Gly Thr Trp Ala Ser
                           930                 935                 940

60     cgc cgc tcc agc tgg aac agc ctg aaa cac aag ccg ccc tca gct gag   2880
       Arg Arg Ser Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu
       945                 950                 955                 960

       cat gag tcc tta ctg tct ggg gag ggt gga ggt agc tgc gtc agg gcc   2928
```

```
     His Glu Ser Leu Leu Ser Gly Glu Gly Gly Gly Ser Cys Val Arg Ala
                     965                 970                 975

 5   tgt gaa ggc gcc cgg gag gag gcg cca act cgc acc gca ccc ctg cat   2976
     Cys Glu Gly Ala Arg Glu Glu Ala Pro Thr Arg Thr Ala Pro Leu His
                 980                 985                 990

     gct cca cac gcg cac cac gcg cac cat gga ccc cac ctg gca cac cgt   3024
10   Ala Pro His Ala His His Ala His His Gly Pro His Leu Ala His Arg
                 995                 1000                1005

     cac cga cac cac cgc cgg act ctg tcc ctt gat acc agg gac tct gtt   3072
     His Arg His His Arg Arg Thr Leu Ser Leu Asp Thr Arg Asp Ser Val
15   1010                1015                1020

     gac ctg gga gag ctg gtg ccc gtg gtg ggt gcc cac tca cgg gcc gct   3120
     Asp Leu Gly Glu Leu Val Pro Val Val Gly Ala His Ser Arg Ala Ala
     1025                1030                1035                1040

20   tgg agg ggg gcg ggt cag gcc cct ggg cac gag gac tgc aat ggc aga   3168
     Trp Arg Gly Ala Gly Gln Ala Pro Gly His Glu Asp Cys Asn Gly Arg
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25   atg ccc aac ata gcc aag gat gtc ttc acc aag atg gat gac cgc cgc   3216
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     Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp Cys Glu Val Arg
35   1090                1095                1100

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     1105                1110                1115                1120

40   ctg tgt cag acc atc att gct cac aag ctt ttt gac tac gtg gtc ttg   3408
     Leu Cys Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu
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45   gcc ttt atc ttc ctc aac tgt atc acc att gct ctg gag aga ccc cag   3456
     Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln
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     att gaa gct ggt agc act gag cgc atc ttc ctc acg gtg tct aac tac   3504
50   Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr
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     atc ttc aca gcc atc ttc gtg ggc gag atg aca ctg aag gtg gtt tct   3552
     Ile Phe Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser
55   1170                1175                1180

     ctg ggc ctg tac ttt ggt gag cag gcg tac ctg cgt agc agc tgg aat   3600
     Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn
     1185                1190                1195                1200

60   gta ctg gat ggt ttc ctg gtc ttt gtg tcc atc atc gat atc gta gtg   3648
     Val Leu Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val
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     tcc gtg gcc tct gct ggg gga gcc aag att ctg ggg gtc ctc cgg gtc   3696
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          Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala
                  1235                1240                1245

          cct ggg ctg aag ctg gtg gta gag acg ctc atc tcc tcc ctc aag ccc    3792
          Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro
 10        1250                1255                1260

          att ggg aac atc gtc ctc atc tgc tgt gcc ttc ttc atc atc ttc ggc    3840
          Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly
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 20       gtg gac acc cga aac atc acc aac cga tct gac tgc gtg gcg gcc aac    3936
          Val Asp Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Val Ala Ala Asn
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 25       Tyr Arg Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala
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          ttg atg tcc ctc ttt gtc ttg gcc tcc aag gac ggc tgg gtg aac atc    4032
          Leu Met Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile
 30            1330                1335                1340

          atg tat aat gga tta gat gct gtt gct gtg gac cag cag cca gtg acg    4080
          Met Tyr Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr
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          aac cac aac ccc tgg atg cta ctg tac ttc att tcg ttc ctg ctc atc    4128
          Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile
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 40       gtc agc ttc ttt gtg ctc aac atg ttt gtg ggc gtg gtc gtg gag aac    4176
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          ttc cac aag tgc cgg cag cac cag gag gct gag gag gcg cgg agg cgt    4224
 45       Phe His Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg
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          gag gag aaa cgg ctg cgg cgc ctg gaa aag aag cgc cgt aag gct cag    4272
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          agg ctg ccc tac tat gct acc tac tgt ccc aca agg ctg ctc atc cac    4320
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 60       tgc ctc aat gtt gtc acc atg tcc ctg gag cac tac aac cag cct aca    4416
          Cys Leu Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
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            Phe Val Leu Glu Ala Val Leu Lys Leu Val Ala Phe Gly Leu Arg Arg
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      10    ttc ttc aag gac cga tgg aac cag ctg gac ctg gcc att gtg ctg ctg    4560
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      25    gac aca gtg gta cag gct ctg ccc cag gtg ggc aac ctg ggc ctg ctc    4752
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            Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe
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      40    gtc tcc aca ggc gat aac tgg aat gga att atg aag gac acc ctg cga    4944
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       acc ctg tgg ctg gac agc gtc tct tta atc atc aag gac tcc ttg gag      5376
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 15                    1780                1785                1790

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       <212> PRT
       <213> Homo sapiens

       <400> 13
 35    Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu
        1               5                10                15

       Lys Met Ala

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INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6   C12N15/12   C07K14/705   C07K16/28   C12N5/10   G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6   C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 04144 A (NEUREX CORP) 9 February 1995	1,2,7, 10-18, 20-22
Y	see abstract; claims 1-10 ---	3,19
X	NOONEY JM (REPRINT) ET AL: "Identifying neuronal non-L Ca2+ channels - more than stamp collecting?" TRENDS IN PHARMACOLOGICAL SCIENCES, 10-1997, 18, 363-371, XP002093637 see page 369, right-hand column - page 370, right-hand column ---	1,2, 10-16, 20-22
	-/--	

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
16 February 1999	09/03/1999

Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl. Fax: (+31-70) 340-3016	Authorized officer Gurdjian, D

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INTERNATIONAL SEARCH REPORT

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	ERTEL S I ET AL: "Low-voltage-activated T-type Cachannels" TRENDS IN PHARMACOLOGICAL SCIENCES, vol. 18, no. 2, February 1997, page 37-42 XP004055849 see page 39, left-hand column, paragraph 4 – page 40, middle column, paragraph 1; table 1 ---	1,2, 10-16, 20-22
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Y	WILSON R ET AL: "2.2 MB OF CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III OF C ELEGANS" NATURE, vol. 368, 3 March 1994, pages 32-38, XP002910426 see abstract	3,19
Y	& EMBL DATABASE Accession number q18840 WILSON R. ET AL. 1996 see the whole document ---	3,19
A	WO 93 04083 A (SALK INST BIOTECH IND) 4 March 1993 see abstract; claims 1-39 ---	1-22
P,X	PEREZ-REYES E ET AL: "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel 'see comments!" NATURE, FEB 26 1998, 391 (6670) P896-900, XP002093639 ENGLAND see the whole document ---	1-15, 20-22
P,X	CRIBBS LL ET AL: "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family." CIRC RES, JUL 13 1998, 83 (1) P103-9, XP002093640 UNITED STATES see the whole document -----	1-22

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INTERNATIONAL SEARCH REPORT

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